

## SEQUENCE LISTING

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INSERM

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pathogenic strains of the Neisseria genus

<130> BET 99/0918

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<150> FR 98 13 893

<151> 1998-10-30

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<170> PatentIn Ver. 2.1

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*Patent # 3/A*

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 <213> Neisseria meningitidis  
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Met	Arg	Thr	Thr	Pro	Thr	Phe	Pro	Thr	Lys	Thr	Phe	Lys	Pro	Ala	Ala	
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Met	Ala	Leu	Ala	Val	Ala	Thr	Thr	Leu	Ser	Ala	Cys	Leu	Gly	Gly	Gly	
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ggc	ggc	act	tct	gcg	ccc	gac	ttc	aat	gca	ggc	ggc	acc	ggg	atc	ggc	144
Gly	Gly	Thr	Ser	Ala	Pro	Asp	Phe	Asn	Ala	Gly	Gly	Thr	Gly	Ile	Gly	
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agc	aac	agc	aga	gca	aca	aca	gcg	aaa	tca	gca	gca	gta	tct	tac	gcc	192
Ser	Asn	Ser	Arg	Ala	Thr	Thr	Ala	Lys	Ser	Ala	Ala	Val	Ser	Tyr	Ala	
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Gly	Ile	Lys	Asn	Glu	Met	Cys	Lys	Asp	Arg	Ser	Met	Leu	Cys	Ala	Gly	
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Arg	Asp	Asp	Val	Ala	Val	Thr	Asp	Arg	Asp	Ala	Lys	Ile	Asn	Ala	Pro	
			85					90						95		
ccc	ccg	aat	ctg	cat	acc	gga	gac	ttt	aca	aac	cca	aat	gac	gca	tac	336
Pro	Pro	Asn	Leu	His	Thr	Gly	Asp	Phe	Thr	Asn	Pro	Asn	Asp	Ala	Tyr	
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Lys	Asn	Leu	Ile	Asn	Leu	Lys	Pro	Ala	Ile	Glu	Ala	Gly	Tyr	Thr	Gly	
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Arg	Gly	Val	Glu	Val	Gly	Ile	Val	Asp	Thr	Gly	Glu	Ser	Val	Gly	Ser	
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ata	tcc	ttt	ccc	gaa	ctg	tat	ggc	aga	aaa	gaa	cac	ggc	tat	aac	gaa	480
Ile	Ser	Phe	Pro	Glu	Leu	Tyr	Gly	Arg	Lys	Glu	His	Gly	Tyr	Asn	Glu	
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Asn	Tyr	Lys	Asn	Tyr	Thr	Ala	Tyr	Met	Arg	Lys	Glu	Ala	Pro	Glu	Asp	
			165					170						175		
gga	ggc	ggg	aaa	gac	att	aaa	gct	tct	ttc	gac	gat	gag	gcc	gtt	ata	576
Gly	Gly	Gly	Lys	Asp	Ile	Lys	Ala	Ser	Phe	Asp	Asp	Glu	Ala	Val	Ile	
			180					185					190			
gag	act	gaa	gca	aag	ccg	acg	gat	atc	cgc	cac	gta	aaa	gaa	atc	gga	624
Glu	Thr	Glu	Ala	Lys	Pro	Thr	Asp	Ile	Arg	His	Val	Lys	Glu	Ile	Gly	
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acg cat gat gga acc aag aac gaa ata atg tct gca gcc atc cgc aat	768
Thr His Asp Gly Thr Lys Asn Glu Ile Met Ser Ala Ala Ile Arg Asn	
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Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser	
260 265 270	
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Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp His Phe Gln Ile Ala	
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Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Ala Tyr Ser Gly Gly	
290 295 300	
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Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly	
305 310 315 320	
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Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser	
325 330 335	
gca agc aat gac gca caa gct cag ccc aac aca ctg acc cta ttg cca	1056
Ala Ser Asn Asp Ala Gln Ala Gln Pro Asn Thr Leu Thr Leu Leu Pro	
340 345 350	
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Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val	
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Asp Arg Ser Gly Glu Lys Phe Asn Gly Ser Asn His Cys Gly Ile Thr	
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gcc atg tgg tgc cta tcg gca ccc tat gaa gca agc gtc cgt ttc acc	1200
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Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile	
405 410 415	
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Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser	
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Asn Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly	
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Ala Val Gly Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly	
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Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile	
485 490 495	
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Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu	
500 505 510	
cac ggc aac aac acc tat acg ggc aaa acc att atc gaa ggc ggt tcg	1584
His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser	
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ctg gtg ttg tac ggc aac aac aaa tcg gat atg cgc gtc gaa acc aaa	1632
Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys	
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Gly Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser	
545 550 555 560	
gac ggc att gtc tat ctg gca gat acc gac cga tcc ggc gca aac gaa	1728
Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Arg Ser Gly Ala Asn Glu	
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acc gtg cac atc aaa ggc gat ctg cag ctg ggc ggc gaa ggt acg ctg	1776
Thr Val His Ile Lys Gly Asp Leu Gln Leu Gly Gly Glu Gly Thr Leu	
580 585 590	
tac aca cgt ttg ggc aaa ctg ctg aaa gtg gac ggt acg gcg atg acc	1824
Tyr Thr Arg Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Met Thr	
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Gly Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu	
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Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr	
660 665 670	
ctg tcc tat tat gtc cgt cgc ggc aat gcg gca cgg act gct tcg gca	2064
Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala	
675 680 685	
gcg gca cat tcc gcg ccc gcc ggt ctg aaa cac gcc gta gaa cag gcc	2112
Ala Ala His Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly	
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tcc gca aca ccc gag acg gtt gaa act gcg gcc gcc gac cgc aca gat Ser Ala Thr Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp 725 730 735	2208
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gta cag cat gcg aat gcc gcc gac ggt gta cgc atc ttc aac agt ctc Val Gln His Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu 755 760 765	2304
gcc gct acc gtc tat gcc gac agt acc gcc gcc cat gcc gat atg cag Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln 770 775 780	2352
gga cgc cgg ctg aaa gcc gta tgc gac ggg ttg gac cac aac gct acg Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Ala Thr 785 790 795 800	2400
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atg gga cac agc aca tgg agc gaa aac agt gca aat gca aaa acc gac Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp 850 855 860	2592
agc att agt ctg ttt gca ggc ata cgg cac gat gcg ggc gat atc gcc Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly 865 870 875 880	2640
tat ctc aaa gcc ctg ttc tcc tac gga cgc tac aaa aac agc atc agc Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser 885 890 895	2688
cgc agc acc ggt gcg gac gaa cat gcg gaa gcc agc gtc aac gcc acg Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr 900 905 910	2736
ctg atg cag ctg ggc gca ctg ggc ggt gtc aac gtt ccg ttt gcc gca Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala 915 920 925	2784
acg gga gat ttg acg gtc gaa gcc ggt ctg cgc tac gac ctg ctc aaa Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys 930 935 940	2832

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<213> Neisseria meningitidis
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20					25					30									
Gly	Gly	Thr	Ser	Ala	Pro	Asp	Phe	Asn	Ala	Gly	Gly	Thr	Gly	Ile	Gly				
35					40					45									
Ser	Asn	Ser	Arg	Ala	Thr	Thr	Ala	Lys	Ser	Ala	Ala	Val	Ser	Tyr	Ala				
50					55					60									
Gly	Ile	Lys	Asn	Glu	Met	Cys	Lys	Asp	Arg	Ser	Met	Leu	Cys	Ala	Gly				
65					70					75					80				
Arg	Asp	Asp	Val	Ala	Val	Thr	Asp	Arg	Asp	Ala	Lys	Ile	Asn	Ala	Pro				
85					90					95									
Pro	Pro	Asn	Leu	His	Thr	Gly	Asp	Phe	Thr	Asn	Pro	Asn	Asp	Ala	Tyr				
100					105					110									

Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly  
 115 120 125  
 Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser  
 130 135 140  
 Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu  
 145 150 155 160  
 Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp  
 165 170 175  
 Gly Gly Gly Lys Asp Ile Lys Ala Ser Phe Asp Asp Glu Ala Val Ile  
 180 185 190  
 Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly  
 195 200 205  
 His Ile Asp Val Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly  
 210 215 220  
 Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn  
 225 230 235 240  
 Thr His Asp Gly Thr Lys Asn Glu Ile Met Ser Ala Ala Ile Arg Asn  
 245 250 255  
 Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser  
 260 265 270  
 Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp His Phe Gln Ile Ala  
 275 280 285  
 Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Ala Tyr Ser Gly Gly  
 290 295 300  
 Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly  
 305 310 315 320  
 Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser  
 325 330 335  
 Ala Ser Asn Asp Ala Gln Ala Gln Pro Asn Thr Leu Thr Leu Leu Pro  
 340 345 350  
 Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val  
 355 360 365  
 Asp Arg Ser Gly Glu Lys Phe Asn Gly Ser Asn His Cys Gly Ile Thr  
 370 375 380  
 Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr  
 385 390 395 400  
 Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile  
 405 410 415  
 Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser  
 420 425 430

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Asn	Asp	Asn	Leu	Arg	Thr	Thr	Leu	Leu	Thr	Thr	Ala	Gln	Asp	Ile	Gly	435	440	445
Ala	Val	Gly	Val	Asp	Ser	Lys	Phe	Gly	Trp	Gly	Leu	Leu	Asp	Ala	Gly	450	455	460
Lys	Ala	Met	Asn	Gly	Pro	Ala	Ser	Phe	Pro	Phe	Gly	Asp	Phe	Thr	Ala	465	470	475
Asp	Thr	Lys	Gly	Thr	Ser	Asp	Ile	Ala	Tyr	Ser	Phe	Arg	Asn	Asp	Ile	485	490	495
Ser	Gly	Thr	Gly	Gly	Leu	Ile	Lys	Lys	Gly	Gly	Ser	Gln	Leu	Gln	Leu	500	505	510
His	Gly	Asn	Asn	Thr	Tyr	Thr	Gly	Lys	Thr	Ile	Ile	Glu	Gly	Gly	Ser	515	520	525
Leu	Val	Leu	Tyr	Gly	Asn	Asn	Lys	Ser	Asp	Met	Arg	Val	Glu	Thr	Lys	530	535	540
Gly	Ala	Leu	Ile	Tyr	Asn	Gly	Ala	Ala	Ser	Gly	Gly	Ser	Leu	Asn	Ser	545	550	555
Asp	Gly	Ile	Val	Tyr	Leu	Ala	Asp	Thr	Asp	Arg	Ser	Gly	Ala	Asn	Glu	565	570	575
Thr	Val	His	Ile	Lys	Gly	Asp	Leu	Gln	Leu	Gly	Gly	Glu	Gly	Thr	Leu	580	585	590
Tyr	Thr	Arg	Leu	Gly	Lys	Leu	Leu	Lys	Val	Asp	Gly	Thr	Ala	Met	Thr	595	600	605
Gly	Gly	Lys	Leu	Tyr	Met	Ser	Ala	Arg	Gly	Lys	Gly	Ala	Gly	Tyr	Leu	610	615	620
Asn	Arg	Thr	Gly	Gln	Arg	Val	Pro	Phe	Leu	Ser	Ala	Ala	Lys	Ile	Gly	625	630	635
Arg	Asp	Tyr	Ser	Phe	Phe	Thr	Asn	Ile	Glu	Thr	Asp	Gly	Gly	Leu	Leu	645	650	655
Ala	Ser	Leu	Asp	Ser	Val	Glu	Lys	Thr	Ala	Gly	Ser	Glu	Gly	Asp	Thr	660	665	670
Leu	Ser	Tyr	Tyr	Val	Arg	Arg	Gly	Asn	Ala	Ala	Arg	Thr	Ala	Ser	Ala	675	680	685
Ala	Ala	His	Ser	Ala	Pro	Ala	Gly	Leu	Lys	His	Ala	Val	Glu	Gln	Gly	690	695	700
Gly	Ser	Asn	Leu	Glu	Asn	Leu	Met	Val	Glu	Leu	Asp	Ala	Ser	Glu	Ser	705	710	715
Ser	Ala	Thr	Pro	Glu	Thr	Val	Glu	Thr	Ala	Ala	Ala	Asp	Arg	Thr	Asp	725	730	735
Met	Pro	Gly	Ile	Arg	Pro	Tyr	Gly	Ala	Thr	Phe	Arg	Ala	Ala	Ala	Ala	740	745	750

008304133-081604

Val Gln His Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu  
755 760 765

Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln  
770 775 780

Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Ala Thr  
785 790 795 800

Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu  
805 810 815

Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly  
820 825 830

Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly  
835 840 845

Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp  
850 855 860

Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly  
865 870 875 880

Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser  
885 890 895

Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr  
900 905 910

Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala  
915 920 925

Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys  
930 935 940

Gln Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn  
945 950 955 960

Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser  
965 970 975

Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu  
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Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly  
995 1000 1005

Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr  
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Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp  
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His Ser Gly Arg Val Gly Val Gly Tyr Arg Phe  
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gca ggt tgc ggc tca atc aat aat gta acc gtt tcc gac cag aaa ctt 96
Ala Gly Cys Gly Ser Ile Asn Asn Val Thr Val Ser Asp Gln Lys Leu
             20             25             30

cag gaa cgt gcc gcg ttt gcc ttg ggc gtc agc caa aat gcc gta aaa 144
Gln Glu Arg Ala Ala Phe Ala Leu Gly Val Ser Gln Asn Ala Val Lys
             35             40             45

atc agc aac cgc agc aat gaa agc ata cgc atc aac ttt acc gca act 192
Ile Ser Asn Arg Ser Asn Glu Ser Ile Arg Ile Asn Phe Thr Ala Thr
             50             55             60

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Val Gly Lys Arg Val Ser Gln Cys Tyr Val Thr Ser Val Ile Ser Thr
             65             70             75             80

atc ggc gtt acc acc tcc gat gca att tgt ttg gga ggc gga acg cac 288
Ile Gly Val Thr Thr Ser Asp Ala Ile Cys Leu Gly Gly Gly Thr His
             85             90             95

aaa ggc aaa agt caa tgc aat gct ttg ctt aaa gcg gca ggc cgt tgc 336
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<213> Neisseria meningitidis

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Gln Glu Arg Ala Ala Phe Ala Leu Gly Val Ser Gln Asn Ala Val Lys
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Ile Ser Asn Arg Ser Asn Glu Ser Ile Arg Ile Asn Phe Thr Ala Thr

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Ile Gly Val Thr Thr Ser Asp Ala Ile Cys Leu Gly Gly Gly Thr His				
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Lys Gly Lys Ser Gln Cys Asn Ala Leu Leu Lys Ala Ala Gly Arg Cys				
	100		105	110

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Leu Leu Thr Glu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro	
20 25 30	
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Leu Phe Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu	
35 40 45	
ttt tat tgg ggc ggc acc aaa tgg gtg atg cag att gtg att atg ttt	192
Phe Tyr Ser Gly Gly Thr Lys Ser Val Met Gln Ile Val Ile Met Phe	
50 55 60	
atg ttt tcc att ttg ttt gga atc atg aac gat gtg ggg ctg ttc	240
Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe	
65 70 75 80	
cgt ccg atg ata ggc ggt ttg att aag ctg act cgg ggt aat atc gtg	288
Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val	
85 90 95	
gca gtg agt gtg ggg acg gtc ttg gtg tgg gtg ggc cag ttg gac	336
Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp	
100 105 110	
ggg gcg ggt gcg acg acg ttt tta ttg gtc gtc ccc gcc ctt ttg ccg	384
Gly Ala Gly Ala Thr Thr Phe Leu Leu Val Val Pro Ala Leu Leu Pro	
115 120 125	
ctt tac aag cgt ctg cat atg aat cct tac ctg ctg ttt ttg ctg ctg	432
Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu	
130 135 140	
act tcc agt gcg gga ttg att aac ctt ctg ccg tgg ggc ggg ccg acc	480

09830433 081601

Thr	Ser	Ser	Ala	Gly	Leu	Ile	Asn	Leu	Leu	Pro	Trp	Gly	Gly	Pro	Thr	
145					150					155					160	
ggg	cgg	gtt	gca	agc	gtg	ttg	ggc	gca	gat	gtg	ggc	gaa	ttg	tat	aaa	528
Gly	Arg	Val	Ala	Ser	Val	Leu	Gly	Ala	Asp	Val	Gly	Glu	Leu	Tyr	Lys	
				165					170					175		
cct	ttg	ttg	acg	gtg	caa	att	atc	ggc	gtg	gtg	ttt	atc	ctt	gcg	ctg	576
Pro	Leu	Leu	Thr	Val	Gln	Ile	Ile	Gly	Val	Val	Phe	Ile	Leu	Ala	Leu	
				180				185					190			
tcc	ctg	ctt	ttg	ggc	gtg	cgt	gaa	aaa	agg	cgg	att	gtc	cgg	gag	ttg	624
Ser	Leu	Leu	Leu	Gly	Val	Arg	Glu	Lys	Arg	Arg	Ile	Val	Arg	Glu	Leu	
			195				200					205				
ggc	gcg	ttg	ccc	gcc	gtg	gcg	gat	ttg	ata	aag	ccg	gtg	ccc	ttg	tcg	672
Gly	Ala	Leu	Pro	Ala	Val	Ala	Asp	Leu	Ile	Lys	Pro	Val	Pro	Leu	Ser	
			210			215					220					
gaa	gaa	gaa	caa	aaa	ttg	gcg	cgt	ccg	aaa	ctg	ttt	tgg	tgg	aat	gtc	720
Glu	Glu	Glu	Gln	Lys	Leu	Ala	Arg	Pro	Lys	Leu	Phe	Trp	Trp	Asn	Val	
					230					235					240	
ctg	ctg	ttt	ttg	gcg	gcg	atg	agc	ctg	ctt	ttt	tcg	ggc	atc	ttc	ccg	768
Leu	Leu	Phe	Leu	Ala	Ala	Met	Ser	Leu	Leu	Phe	Ser	Gly	Ile	Phe	Pro	
				245					250					255		
ccg	ggc	tat	gta	ttt	atg	ctg	gct	gca	acg	gcg	gcg	ttg	ctt	ttg	aat	816
Pro	Gly	Tyr	Val	Phe	Met	Leu	Ala	Ala	Thr	Ala	Ala	Leu	Leu	Leu	Asn	
			260					265					270			
tac	cgc	agc	ccg	cag	gaa	cag	atg	gag	cgg	att	tat	gcc	cac	gcc	ggc	864
Tyr	Arg	Ser	Pro	Gln	Glu	Gln	Met	Glu	Arg	Ile	Tyr	Ala	His	Ala	Gly	
			275				280					285				
ggc	gcg	gtg	atg	atg	gcg	tcc	att	att	ttg	gcg	gca	ggc	acg	ttt	ttg	912
Gly	Ala	Val	Met	Met	Ala	Ser	Ile	Ile	Leu	Ala	Ala	Gly	Thr	Phe	Leu	
			290			295					300					
ggg	att	ttg	aag	ggc	gcg	ggg	atg	ttg	gac	gcg	att	tcc	aaa	gac	att	960
Gly	Ile	Leu	Lys	Gly	Ala	Gly	Met	Leu	Asp	Ala	Ile	Ser	Lys	Asp	Ile	
				310					315					320		
gtg	cat	atc	ctg	ccg	gac	gcg	ctg	ctg	ccc	tat	ctg	cat	att	gcc	atc	1008
Val	His	Ile	Leu	Pro	Asp	Ala	Leu	Leu	Pro	Tyr	Leu	His	Ile	Ala	Ile	
				325					330					335		
ggc	gtg	ttg	ggc	att	ccg	ctt	gag	ttg	gtt	ctg	agt	acg	gac	gct	tat	1056
Gly	Val	Leu	Gly	Ile	Pro	Leu	Glu	Leu	Val	Leu	Ser	Thr	Asp	Ala	Tyr	
			340				345						350			
tat	ttc	gga	ctg	ttt	ccg	att	gtg	gag	cag	att	acc	tcg	cag	gcg	ggc	1104
Tyr	Phe	Gly	Leu	Phe	Pro	Ile	Val	Glu	Gln	Ile	Thr	Ser	Gln	Ala	Gly	
			355				360					365				
gtg	gcg	ccc	gaa	gca	gca	ggc	tat	gcg	atg	ttg	atc	ggc	agt	atc	gtc	1152
Val	Ala	Pro	Glu	Ala	Ala	Gly	Tyr	Ala	Met	Leu	Ile	Gly	Ser	Ile	Val	
			370			375					380					
ggc	act	ttt	gtt	acg	ccg	ctt	tcg	ccg	gct	ttg	tgg	atg	ggc	ttg	ggc	1200

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Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly  
 385 390 395 400  
 ttg gcg aaa ttg tcg atg ggc aaa cac atc cgt tat tcg ttt ttt tgg 1248  
 Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp  
 405 410 415  
 gcg tgg ggt ttg tcg ctg gcg ata ttg gcc agt tcg ata gcg gca gga 1296  
 Ala Trp Gly Leu Ser Leu Ala Ile Leu Ala Ser Ser Ile Ala Ala Gly  
 420 425 430  
 atc gtg cct ctg ccg taa 1314  
 Ile Val Pro Leu Pro  
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 <213> Neisseria meningitidis

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 35 40 45  
 Phe Tyr Ser Gly Gly Thr Lys Ser Val Met Gln Ile Val Ile Met Phe  
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 Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe  
 65 70 75 80  
 Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val  
 85 90 95  
 Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp  
 100 105 110  
 Gly Ala Gly Ala Thr Thr Phe Leu Leu Val Val Pro Ala Leu Leu Pro  
 115 120 125  
 Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu  
 130 135 140  
 Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Trp Gly Gly Pro Thr  
 145 150 155 160  
 Gly Arg Val Ala Ser Val Leu Gly Ala Asp Val Gly Glu Leu Tyr Lys  
 165 170 175  
 Pro Leu Leu Thr Val Gln Ile Ile Gly Val Val Phe Ile Leu Ala Leu  
 180 185 190  
 Ser Leu Leu Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu  
 195 200 205

000043 081601

Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Val Pro Leu Ser  
 210 215 220

Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val  
 225 230 235 240

Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro  
 245 250 255

Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Leu Asn  
 260 265 270

Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly  
 275 280 285

Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu  
 290 295 300

Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Ile  
 305 310 315 320

Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile  
 325 330 335

Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr  
 340 345 350

Tyr Phe Gly Leu Phe Pro Ile Val Glu Gln Ile Thr Ser Gln Ala Gly  
 355 360 365

Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val  
 370 375 380

Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly  
 385 390 395 400

Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp  
 405 410 415

Ala Trp Gly Leu Ser Leu Ala Ile Leu Ala Ser Ser Ile Ala Ala Gly  
 420 425 430

Ile Val Pro Leu Pro  
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 <213> Neisseria meningitidis

<220>  
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 <222> (1)..(1152)

00000433 001001

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act tat ctg tat caa aag ccc aag ctc ttt aaa gga gcg gtt cgg aat 96  
Thr Tyr Leu Tyr Gln Lys Pro Lys Leu Phe Lys Gly Ala Val Arg Asn  
20 25 30

ctc gaa gcc gca tct tgt aaa tat atc aac gag ata tac caa cga gca 144  
Leu Glu Ala Ala Ser Cys Lys Tyr Ile Asn Glu Ile Tyr Gln Arg Ala  
35 40 45

gac cca acc gca ccg ctg ttt cat ctg cgt aaa aaa ggc gca atc gtt 192  
Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val  
50 55 60

cct aaa gaa gaa tac gtc gaa agt ttc gac gat ttg ggc aaa act cgc 240  
Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg  
65 70 75 80

tac cgt ttt att aaa tcc gtt atc tac gaa cat atg aag aat ggt gcg 288  
Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala  
85 90 95

tcg tta gtc tat aac cat att aac aac gag ccg ttt tca gac cat atc 336  
Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile  
100 105 110

gcc cgt caa gtc gcc cgc ttt gcc ggc gca cat act att gtt agt gga 384  
Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly  
115 120 125

tat ctt gct ttt ggc agc gac gaa tct tat aaa aac cat tgg gat acc 432  
Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr  
130 135 140

cgc gat gtg tat gcc atc cag ctt ttc ggc aag aaa cgt tgg caa ctt 480  
Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu  
145 150 155 160

act gcc cct gat ttc cct atg cca ttg tat atg caa cag act aaa gat 528  
Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp  
165 170 175

act gat att tcc att cct gaa cat atc gat atg gat att atc ctt gaa 576  
Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu  
180 185 190

gca ggt gat gtc ctc tac atc cca cgc ggt tgg tgg cac aga cct atc 624  
Ala Gly Asp Val Leu Tyr Ile Pro Arg Gly Trp Trp His Arg Pro Ile  
195 200 205

ccg ctc ggc tgt gaa acc ttc cac ttc gct gtc ggt acc ttc ccg ccc 672  
Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro  
210 215 220

aac ggc tat aat tac ctc gag tgg cta atg aag aaa ttc ccc acg ata 720  
Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile  
225 230 235 240

gaa agt ctg cgc cac agt ttc tca gac tgg gag caa gat agg acg cgt 768  
Glu Ser Leu Arg His Ser Phe Ser Asp Trp Glu Gln Asp Arg Thr Arg

00000433 001601

	245	250	255	
atc aac gat act gcc gca caa att gct gcc atg att gcc gac ccc gtc				816
Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val				
	260	265	270	
aat tac gaa gcc ttc agt gaa gac ttc ctc ggc aaa gaa cgc acc gat				864
Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp				
	275	280	285	
acc gct ttt cat ctc gaa cag ttc gcg aat ccc aac gct act ccg ctt				912
Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu				
	290	295	300	
tca gac gac gtc agg ttg aga cta aat gcc aat aat ttg gat acg ttg				960
Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu				
	305	310	315	320
gaa aag gga tat ttg att ggg aat ggg atg aag ata agc gta gat gaa				1008
Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu				
	325	330	335	
ttg ggg aaa aaa gtg tta gaa cac atc ggt aag aat gaa ccg tta ttg				1056
Leu Gly Lys Lys Val Leu Glu His Ile Gly Lys Asn Glu Pro Leu Leu				
	340	345	350	
ttg aaa aat cta ctg gtt aac ttc aat cag gga aaa cat gaa gaa gtt				1104
Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Gly Lys His Glu Glu Val				
	355	360	365	
agg aag ttg att tat cag ttg ata gag tta gat ttt ctg gaa ctt ttg				1152
Arg Lys Leu Ile Tyr Gln Leu Ile Glu Leu Asp Phe Leu Glu Leu Leu				
	370	375	380	
tga				1155

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 Leu Glu Ala Ala Ser Cys Lys Tyr Ile Asn Glu Ile Tyr Gln Arg Ala  
 35 40 45  
 Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val  
 50 55 60  
 Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg  
 65 70 75 80  
 Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala  
 85 90 95

00000433 001601

Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile  
100 105 110

Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly  
115 120 125

Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr  
130 135 140

Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu  
145 150 155 160

Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp  
165 170 175

Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu  
180 185 190

Ala Gly Asp Val Leu Tyr Ile Pro Arg Gly Trp Trp His Arg Pro Ile  
195 200 205

Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro  
210 215 220

Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile  
225 230 235 240

Glu Ser Leu Arg His Ser Phe Ser Asp Trp Glu Gln Asp Arg Thr Arg  
245 250 255

Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val  
260 265 270

Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp  
275 280 285

Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu  
290 295 300

Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu  
305 310 315 320

Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu  
325 330 335

Leu Gly Lys Lys Val Leu Glu His Ile Gly Lys Asn Glu Pro Leu Leu  
340 345 350

Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Gly Lys His Glu Glu Val  
355 360 365

Arg Lys Leu Ile Tyr Gln Leu Ile Glu Leu Asp Phe Leu Glu Leu Leu  
370 375 380

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- <211> 717
- <212> DNA
- <213> Neisseria meningitidis
- <220>

09030433 081601

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Met	Asn	Arg	Pro	Lys	Gln	Pro	Phe	Phe	Arg	Pro	Glu	Val	Ala	Val	Ala	
1				5					10					15		
cgc	caa	acc	agc	ctg	acg	ggg	aaa	gtg	att	ctg	aca	cga	ccg	ttg	tca	96
Arg	Gln	Thr	Ser	Leu	Thr	Gly	Lys	Val	Ile	Leu	Thr	Arg	Pro	Leu	Ser	
			20					25					30			
ttt	tcc	cta	tgg	acg	aca	ttt	gca	tcg	ata	tct	gcg	tta	ttg	att	atc	144
Phe	Ser	Leu	Trp	Thr	Thr	Phe	Ala	Ser	Ile	Ser	Ala	Leu	Leu	Ile	Ile	
		35					40					45				
ctg	ttt	tgg	ata	ttt	ggg	aac	tat	acg	cga	aag	aca	aca	gtg	gag	gga	192
Leu	Phe	Leu	Ile	Phe	Gly	Asn	Tyr	Thr	Arg	Lys	Thr	Thr	Val	Glu	Gly	
		50				55					60					
caa	att	tta	cct	gca	tcg	ggc	gta	atc	agg	gtg	tat	gca	ccg	gat	acg	240
Gln	Ile	Leu	Pro	Ala	Ser	Gly	Val	Ile	Arg	Val	Tyr	Ala	Pro	Asp	Thr	
65					70					75					80	
ggg	aca	att	aca	gcg	aaa	ttc	gtg	gaa	gat	gga	gaa	aag	gtt	aag	gct	288
Gly	Thr	Ile	Thr	Ala	Lys	Phe	Val	Glu	Asp	Gly	Glu	Lys	Val	Lys	Ala	
				85					90					95		
ggc	gac	aag	cta	ttt	gcg	ctt	tcg	acc	tca	cgt	ttc	ggc	gca	gga	gat	336
Gly	Asp	Lys	Leu	Phe	Ala	Leu	Ser	Thr	Ser	Arg	Phe	Gly	Ala	Gly	Asp	
			100					105					110			
agc	gtg	cag	cag	cag	ttg	aaa	acg	gag	gca	gtt	ttg	aag	aaa	acg	ttg	384
Ser	Val	Gln	Gln	Gln	Leu	Lys	Thr	Glu	Ala	Val	Leu	Lys	Lys	Thr	Leu	
		115					120					125				
gca	gaa	cag	gaa	ctg	ggg	cgt	ctg	aag	ctg	ata	cac	ggg	aat	gaa	acg	432
Ala	Glu	Gln	Glu	Leu	Gly	Arg	Leu	Lys	Leu	Ile	His	Gly	Asn	Glu	Thr	
		130				135					140					
cgc	agc	ctt	aaa	gca	act	gtc	gaa	cgt	ttg	gaa	aac	cag	aaa	ctc	cat	480
Arg	Ser	Leu	Lys	Ala	Thr	Val	Glu	Arg	Leu	Glu	Asn	Gln	Lys	Leu	His	
145						150				155					160	
att	tcg	caa	cag	ata	gac	ggg	cag	aaa	agg	cgc	att	aga	ctt	gcg	gaa	528
Ile	Ser	Gln	Gln	Ile	Asp	Gly	Gln	Lys	Arg	Arg	Ile	Arg	Leu	Ala	Glu	
				165					170					175		
gaa	atg	ttg	cag	aaa	tat	cgt	ttc	cta	tcc	gcc	aat	gat	gca	gtg	cca	576
Glu	Met	Leu	Gln	Lys	Tyr	Arg	Phe	Leu	Ser	Ala	Asn	Asp	Ala	Val	Pro	
			180					185					190			
aaa	caa	gaa	atg	atg	aat	gtc	aag	gca	gag	ctt	tta	gag	cag	aaa	gcc	624
Lys	Gln	Glu	Met	Met	Asn	Val	Lys	Ala	Glu	Leu	Leu	Glu	Gln	Lys	Ala	
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 <213> Neisseria meningitidis

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 Phe Ser Leu Trp Thr Thr Phe Ala Ser Ile Ser Ala Leu Leu Ile Ile  
 35 40 45  
 Leu Phe Leu Ile Phe Gly Asn Tyr Thr Arg Lys Thr Thr Val Glu Gly  
 50 55 60  
 Gln Ile Leu Pro Ala Ser Gly Val Ile Arg Val Tyr Ala Pro Asp Thr  
 65 70 75 80  
 Gly Thr Ile Thr Ala Lys Phe Val Glu Asp Gly Glu Lys Val Lys Ala  
 85 90 95  
 Gly Asp Lys Leu Phe Ala Leu Ser Thr Ser Arg Phe Gly Ala Gly Asp  
 100 105 110  
 Ser Val Gln Gln Gln Leu Lys Thr Glu Ala Val Leu Lys Lys Thr Leu  
 115 120 125  
 Ala Glu Gln Glu Leu Gly Arg Leu Lys Leu Ile His Gly Asn Glu Thr  
 130 135 140  
 Arg Ser Leu Lys Ala Thr Val Glu Arg Leu Glu Asn Gln Lys Leu His  
 145 150 155 160  
 Ile Ser Gln Gln Ile Asp Gly Gln Lys Arg Arg Ile Arg Leu Ala Glu  
 165 170 175  
 Glu Met Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro  
 180 185 190  
 Lys Gln Glu Met Met Asn Val Lys Ala Glu Leu Leu Glu Gln Lys Ala  
 195 200 205  
 Lys Leu Asp Ala Tyr Arg Arg Glu Glu Val Gly Leu Leu Gln Glu Ile  
 210 215 220  
 Arg Thr Gln Asn Leu Thr Leu Ala Ser Leu Pro Gln Ala Ala  
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003043-04604

<220>

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gcc tac ggc cga gaa gaa gcc ggg ctg ctt cag gaa atc cgc acg cag	96
Ala Tyr Gly Arg Glu Glu Ala Gly Leu Leu Gln Glu Ile Arg Thr Gln	
20 25 30	
aat ctg aca ttg gcc agc ctc ccc aaa cgg cat gag aca gaa caa agc	144
Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser	
35 40 45	
cag ctt gaa cgc acc atg gcc gat att tct caa gaa gtt ttg gat ttt	192
Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe	
50 55 60	
gaa atg cgc tct gaa caa atc atc cgt gca gga cgg tcg ggt tat ata	240
Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile	
65 70 75 80	
gca ata ccg aac gtc gaa gtc gga cag cag gtt gat cct tcc aaa ctg	288
Ala Ile Pro Asn Val Glu Val Gly Gln Gln Val Asp Pro Ser Lys Leu	
85 90 95	
ctc ttg agc att gtt ccc gaa cgt acc gag cta tat gcc cat cta tat	336
Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr	
100 105 110	
atc ccc agc agt gca gca ggc ttt atc aag ccg aaa gac aag gtt gtc	384
Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val	
115 120 125	
cta cgt tat cag gca tat ccc tat caa aaa ttc ggg ctt gct tcc ggc	432
Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly	
130 135 140	
agt gtc gta tca gta gca aaa acg gca ctg ggc aga cag gaa ttg tcg	480
Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser	
145 150 155 160	
gga ttg ggc atg gta tcc tcc gat ttg gcg aag agc aac gaa cct gtt	528
Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val	
165 170 175	
tat ctc gtg aaa ata aaa ccc gac aaa cca acc atc act gca tac ggt	576
Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly	
180 185 190	
gag gaa aaa ccg ctg caa atc ggc atg acg ttg gaa gca gac atc ctg	624
Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu	
195 200 205	
cac gag aaa cgg cgg ctg tac gaa tgg gta ttg gag ctg att tat agt	672
His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Leu Ile Tyr Ser	
210 215 220	
atg tcg ggc aaa ctg taa	690
Met Ser Gly Lys Leu	
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09630433-081601

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 <212> PRT  
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 Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser  
 35 40 45  
 Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe  
 50 55 60  
 Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile  
 65 70 75 80  
 Ala Ile Pro Asn Val Glu Val Gly Gln Gln Val Asp Pro Ser Lys Leu  
 85 90 95  
 Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr  
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 Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val  
 115 120 125  
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 130 135 140  
 Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser  
 145 150 155 160  
 Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val  
 165 170 175  
 Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly  
 180 185 190  
 Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu  
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 His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Leu Ile Tyr Ser  
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 Met Ser Gly Lys Leu  
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<221> CDS

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1 5 10 15

ccc ctt aaa acc tta gct gcc gat gaa aac gat gca gaa ctt atc cgt 96  
Pro Leu Lys Thr Leu Ala Ala Asp Glu Asn Asp Ala Glu Leu Ile Arg  
20 25 30

tcc atg cag cgt cag cag cac ata gat gct gaa ttg tta act gat gca 144  
 Ser Met Gln Arg Gln Gln His Ile Asp Ala Glu Leu Leu Thr Asp Ala  
 35 40 45

aat gtc cgt ttc gag caa cca ttg gag aag aac aat tat gtc ctg agt 192  
Asn Val Arg Phe Glu Gln Pro Leu Glu Lys Asn Asn Tyr Val Leu Ser  
50 55 60

Gaa gat gaa aca cgg tgt act cgg gta aat tac att agt tta gat gat 240  
Glu Asp Glu Thr Pro Cys Thr Arg Val Asn Tyr Ile Ser Leu Asp Asp  
65 70 75 80

aag acg gcg cgc aaa ttt tct ttt ctt cct tct gtg ctc atg aaa gaa 288  
Lys Thr Ala Arg Lys Phe Ser Phe Leu Pro Ser Val Leu Met Lys Glu  
85 90 95

aca gct ttt aaa act ggg atg tgt tta ggt tcc aat aat ttg agc agg 336  
Thr Ala Phe Lys Thr Gly Met Cys Leu Gly Ser Asn Asn Leu Ser Arg  
100 105 110

cta caa aaa gcc gcg caa cag ata ctg att gtg cgt ggc tac ctc act 384  
Leu Gln Lys Ala Ala Gln Gln Ile Leu Ile Val Arg Gly Tyr Leu Thr  
115 120 125

tcc caa gct att atc caa cca cag aat atg gat tcc gga att ctg aaa 432  
Ser Gln Ala Ile Ile Gln Pro Gln Asn Met Asp Ser Gly Ile Leu Lys  
130 135 140

tta	cgg	gta	tca	gca	ggc	gaa	atc	agg	gat	atc	cgc	tat	gaa	gaa	aaa	480
Leu	Arg	Val	Ser	Ala	Gly	Glu	Ile	Arg	Asp	Ile	Arg	Tyr	Glu	Glu	Lys	
145					150					155					160	

cgg gat gcg aag tct gcc gag ggc agt att agt gca ttc aat aac aaa 528  
 Arg Asp Ala Lys Ser Ala Glu Gly Ser Ile Ser Ala Phe Asn Asn Lys  
 165 170 175

ctt ccc tta tat agg aac aaa att ctc aat ctt cgc gat gta gag cag 576

Leu	Pro	Leu	Tyr	Arg	Asn	Lys	Ile	Leu	Asn	Leu	Arg	Asp	Val	Glu	Gln		
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Gly	Leu	Glu	Asn	Leu	Arg	Arg	Leu	Pro	Ser	Val	Lys	Thr	Asp	Ile	Gln		
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Gln	Gln	Asn	Lys	Pro	Ile	Arg	Phe	Ser	Ile	Gly	Ile	Asp	Asp	Ala	Gly		
225					230					235					240		
ggc	aaa	acg	acc	ggc	aaa	tat	caa	gga	aat	gtc	gct	tta	tcg	tcc	gat	768	
Gly	Lys	Thr	Thr	Gly	Lys	Tyr	Gln	Gly	Asn	Val	Ala	Leu	Ser	Ser	Asp		
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Asn	Pro	Leu	Gly	Leu	Ser	Asp	Ser	Phe	Tyr	Val	Ser	Tyr	Gly	Arg	Gly		
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Leu	Val	His	Lys	Thr	Asp	Leu	Thr	Ala	Ala	Thr	Gly	Thr	Glu	Thr	Glu		
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Ser	Gly	Ser	Arg	Ser	Tyr	Ser	Val	His	Tyr	Ser	Val	Pro	Val	Lys	Lys		
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Trp	Leu	Phe	Ser	Phe	Asn	His	Asn	Gly	His	Arg	Tyr	His	Glu	Ala	Thr		
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gaa	ggc	tat	tcc	gtc	aat	tac	gat	tac	aac	ggc	aaa	caa	tat	cag	agc	1008	
Glu	Gly	Tyr	Ser	Val	Asn	Tyr	Asp	Tyr	Asn	Gly	Lys	Gln	Tyr	Gln	Ser		
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agc	ctg	gcc	gcc	gag	cgc	atg	ctt	tgg	ccc	ccc	agc	ttt	cct	caa	act	1056	
Ser	Leu	Ala	Ala	Glu	Arg	Met	Leu	Trp	Pro	Pro	Ser	Phe	Pro	Gln	Thr		
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Ser	Val	Arg	Met	Lys	Leu	Trp	Thr	Arg	Gln	Thr	Tyr	Lys	Tyr	Ile	Asp		
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gat	gcc	gaa	atc	gaa	gtg	caa	cgc	cgc	cgc	tct	gca	ggc	tgg	gaa	gcc	1152	
Asp	Ala	Glu	Ile	Glu	Val	Gln	Arg	Arg	Arg	Ser	Ala	Gly	Trp	Glu	Ala		
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Glu	Leu	Arg	His	Arg	Ala	Tyr	Leu	His	Arg	Trp	Gln	Leu	Asp	Gly	Lys		
385					390					395					400		
ttg	tct	tac	aaa	cgc	ggg	acc	ggc	atg	cgc	caa	agt	atg	ccc	gca	cct	1248	
Leu	Ser	Tyr	Lys	Arg	Gly	Thr	Gly	Met	Arg	Gln	Ser	Met	Pro	Ala	Pro		
				405				410					415				
gaa	gaa	aac	ggc	ggc	ggc	ggt	act	att	cca	gcc	aca	tcc	cgt	atg	aaa	atc	1296

0030433 081601

Glu Glu Asn Gly Gly Gly Thr Ile Pro Ala Thr Ser Arg Met Lys Ile  
 420 425 430  
 ata acc gcc gga ttg gat gca gcg gcc ccg tct atg ttg ggc aaa cag 1344  
 Ile Thr Ala Gly Leu Asp Ala Ala Ala Pro Ser Met Leu Gly Lys Gln  
 435 440 445  
 cag ttt ttc tac gca acc gcc att caa gct caa tgg aac aaa acg cct 1392  
 Gln Phe Phe Tyr Ala Thr Ala Ile Gln Ala Gln Trp Asn Lys Thr Pro  
 450 455 460  
 ttg gtt gcc caa gac aag ttg tct atc ggc agc cgc tac acc gtt cgc 1440  
 Leu Val Ala Gln Asp Lys Leu Ser Ile Gly Ser Arg Tyr Thr Val Arg  
 465 470 475 480  
 gga ttt gat ggg gag cag agt ctt ttc gga gag cga ggt ttc tac tgg 1488  
 Gly Phe Asp Gly Glu Gln Ser Leu Phe Gly Glu Arg Gly Phe Tyr Trp  
 485 490 495  
 cag aat act tta act tgg tat ttt cat ccg aac cat cag ttc tat ctc 1536  
 Gln Asn Thr Leu Thr Trp Tyr Phe His Pro Asn His Gln Phe Tyr Leu  
 500 505 510  
 ggt gcg gac tat ggc cgc gta tct ggc gaa agt gca caa tat gta tcg 1584  
 Gly Ala Asp Tyr Gly Arg Val Ser Gly Glu Ser Ala Gln Tyr Val Ser  
 515 520 525  
 ggc aag cag ctg atg ggt gca gtg gtc ggc ttc aga gga ggg cat aaa 1632  
 Gly Lys Gln Leu Met Gly Ala Val Val Gly Phe Arg Gly Gly His Lys  
 530 535 540  
 gta ggc ggt atg ttt gct tat gat ctg ttt gcc ggc aag ccg ctt cat 1680  
 Val Gly Gly Met Phe Ala Tyr Asp Leu Phe Ala Gly Lys Pro Leu His  
 545 550 555 560  
 aaa ccc aaa ggc ttt cag acg acc aac acc gtt tac ggc ttc aac ttg 1728  
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 <212> PRT  
 <213> Neisseria meningitidis

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 Ser Met Gln Arg Gln Gln His Ile Asp Ala Glu Leu Leu Thr Asp Ala  
 35 40 45  
 Asn Val Arg Phe Glu Gln Pro Leu Glu Lys Asn Asn Tyr Val Leu Ser

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50

55

60

Glu Asp Glu Thr Pro Cys Thr Arg Val Asn Tyr Ile Ser Leu Asp Asp  
65 70 75 80

Lys Thr Ala Arg Lys Phe Ser Phe Leu Pro Ser Val Leu Met Lys Glu  
85 90 95

Thr Ala Phe Lys Thr Gly Met Cys Leu Gly Ser Asn Asn Leu Ser Arg  
100 105 110

Leu Gln Lys Ala Ala Gln Gln Ile Leu Ile Val Arg Gly Tyr Leu Thr  
115 120 125

Ser Gln Ala Ile Ile Gln Pro Gln Asn Met Asp Ser Gly Ile Leu Lys  
130 135 140

Leu Arg Val Ser Ala Gly Glu Ile Arg Asp Ile Arg Tyr Glu Glu Lys  
145 150 155 160

Arg Asp Ala Lys Ser Ala Glu Gly Ser Ile Ser Ala Phe Asn Asn Lys  
165 170 175

Leu Pro Leu Tyr Arg Asn Lys Ile Leu Asn Leu Arg Asp Val Glu Gln  
180 185 190

Gly Leu Glu Asn Leu Arg Arg Leu Pro Ser Val Lys Thr Asp Ile Gln  
195 200 205

Ile Ile Pro Ser Glu Glu Glu Gly Lys Ser Asp Leu Gln Ile Lys Trp  
210 215 220

Gln Gln Asn Lys Pro Ile Arg Phe Ser Ile Gly Ile Asp Asp Ala Gly  
225 230 235 240

Gly Lys Thr Thr Gly Lys Tyr Gln Gly Asn Val Ala Leu Ser Ser Asp  
245 250 255

Asn Pro Leu Gly Leu Ser Asp Ser Phe Tyr Val Ser Tyr Gly Arg Gly  
260 265 270

Leu Val His Lys Thr Asp Leu Thr Ala Ala Thr Gly Thr Glu Thr Glu  
275 280 285

Ser Gly Ser Arg Ser Tyr Ser Val His Tyr Ser Val Pro Val Lys Lys  
290 295 300

Trp Leu Phe Ser Phe Asn His Asn Gly His Arg Tyr His Glu Ala Thr  
305 310 315 320

Glu Gly Tyr Ser Val Asn Tyr Asp Tyr Asn Gly Lys Gln Tyr Gln Ser  
325 330 335

Ser Leu Ala Ala Glu Arg Met Leu Trp Pro Pro Ser Phe Pro Gln Thr  
340 345 350

Ser Val Arg Met Lys Leu Trp Thr Arg Gln Thr Tyr Lys Tyr Ile Asp  
355 360 365

Asp Ala Glu Ile Glu Val Gln Arg Arg Arg Ser Ala Gly Trp Glu Ala

09630433.084604

370		375		380
Glu Leu Arg His Arg	Ala Tyr Leu His Arg	Trp Gln Leu Asp Gly Lys		
385	390	395	400	
Leu Ser Tyr Lys Arg	Gly Thr Gly Met Arg	Gln Ser Met Pro Ala Pro		
	405	410	415	
Glu Glu Asn Gly Gly Gly	Thr Ile Pro Ala Thr Ser Arg Met Lys Ile			
	420	425	430	
Ile Thr Ala Gly Leu Asp	Ala Ala Ala Pro Ser Met Leu Gly Lys Gln			
	435	440	445	
Gln Phe Phe Tyr Ala Thr	Ala Ile Gln Ala Gln Trp Asn Lys Thr Pro			
	450	455	460	
Leu Val Ala Gln Asp Lys	Leu Ser Ile Gly Ser Arg Tyr Thr Val Arg			
	465	470	475	480
Gly Phe Asp Gly Glu Gln	Ser Leu Phe Gly Glu Arg Gly Phe Tyr Trp			
	485	490	495	
Gln Asn Thr Leu Thr Trp	Tyr Phe His Pro Asn His Gln Phe Tyr Leu			
	500	505	510	
Gly Ala Asp Tyr Gly Arg	Val Ser Gly Glu Ser Ala Gln Tyr Val Ser			
	515	520	525	
Gly Lys Gln Leu Met Gly	Ala Val Val Gly Phe Arg Gly Gly His Lys			
	530	535	540	
Val Gly Gly Met Phe Ala	Tyr Asp Leu Phe Ala Gly Lys Pro Leu His			
	545	550	555	560
Lys Pro Lys Gly Phe Gln	Thr Thr Asn Thr Val Tyr Gly Phe Asn Leu			
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Asn Tyr Ser Phe				
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- <211> 411
- <212> DNA
- <213> Neisseria meningitidis
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- <221> CDS
- <222> (1) .. (408)

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ctt ttg ctt gtg tgg acg tgc ggt tac cga tac gcc gcc gac aag gcc 96
Leu Leu Leu Val Trp Thr Cys Gly Tyr Arg Tyr Ala Ala Asp Lys Ala
20 25 30

gaa gcg aaa caa acc gcc ctg att gcc acc tat cgg cat tct tct atg 144
Glu Ala Lys Gln Thr Ala Leu Ile Ala Thr Tyr Arg His Ser Ser Met
35 40 45

gtt gcg gcg gaa caa tac gcc ttg cag ctt aaa aaa gcg cag gac gaa 192
Val Ala Ala Glu Gln Tyr Ala Leu Gln Leu Lys Lys Ala Gln Asp Glu
50 55 60

agg cag cgg tgg tac gac ttt tcc caa aaa caa gga aga aag ccc gtg 240
Arg Gln Arg Trp Tyr Asp Phe Ser Gln Lys Gln Gly Arg Lys Pro Val
65 70 75 80

aaa aaa cag tat ccg ccg caa acg aaa aaa gcc gcc tat ctg aaa acc 288
Lys Lys Gln Tyr Pro Pro Gln Thr Lys Lys Ala Gly Tyr Leu Lys Thr
85 90 95

aag gaa gaa ctg ctt gcg gaa ttg gct tgc ctt aaa gcg gaa atg gct 336
Lys Glu Glu Leu Leu Ala Glu Leu Ala Cys Leu Lys Ala Glu Met Ala
100 105 110

gcc cta aaa aag ctc gat gcc tta atc tat ggg aaa gaa gtg cgg cag 384
Ala Leu Lys Lys Leu Asp Ala Leu Ile Tyr Gly Lys Glu Val Arg Gln
115 120 125

aaa gaa cgc aac tcg tcg cag ggt taa 411
Lys Glu Arg Asn Ser Ser Gln Gly
130 135

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<210> 22
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<212> PRT
<213> Neisseria meningitidis

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09630433 081604

Lys Glu Arg Asn Ser Ser Gln Gly  
130 135

<210> . 23

<211> 924

<212> DNA

<213> Neisseria meningitidis

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<221> CDS

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aat aat ttc ggg ttt ttg cgc ctg ccg ctt aat ttt atg ccg tat gaa 96  
Asn Asn Phe Gly Phe Leu Arg Leu Pro Leu Asn Phe Met Pro Tyr Glu  
20 25 30

agt cat gcc gat tgg gtt att acc ggc gtg cct tat gat atg gcg gtt 144  
Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val  
35 40 45

tca ggg cgt tcc ggc gcg cgt ttc ggt cct gaa gcc atc cgg cgc gcc 192  
Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala  
50 55 60

tcc gtc aac ctc gct tgg gag cac cgc agg ttt cca tgg aca ttt gat 240  
Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp  
65 70 75 80

gtg cgc gaa cgc ctg aac att att gat tgc ggc gac ttg gtt ttt tct 288  
Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser  
85 90 95

ttt ggc gac agc agg gat ttt gtc gaa aaa atg gaa gcg cac gcc ggc 336  
Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly  
100 105 110

aaa tta ctt tct tcc ggc aaa cgc tgt ttg agt ttg ggc ggc gac cat 384  
Lys Leu Leu Ser Ser Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His  
115 120 125

ttc att acc ctc ccg ttg ttg cgc gcc cac gcc cgc tat ttc ggc aaa 432  
Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys  
130 135 140

ctc gca ctg att cat ttt gac gcg cac acc gac acc tac gac aac ggc 480  
Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly  
145 150 155 160

agc gaa tac gac cac ggt acg atg ttc tat acc gcc ccc aag gaa ggc 528  
Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly  
165 170 175

ctc atc gac ccg tcc cgt tcc gta caa atc ggc ata cgt acc gaa cac 576

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T09T00-EEH0E060

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Ser	Lys	Lys	Leu	Pro	Phe	Thr	Val	Leu	Thr	Ala	Pro	Gln	Val	Asn	Glu		
		195					200					205					
gac	agt	gtt	gaa	gag	acc	gtc	cgt	aaa	atc	aaa	gaa	acc	gtc	ggc	aat	672	
Asp	Ser	Val	Glu	Glu	Thr	Val	Arg	Lys	Ile	Lys	Glu	Thr	Val	Gly	Asn		
		210				215					220						
atg	ccc	gtt	tac	ctg	act	ttc	gac	ata	gac	tgc	ctc	gac	ccg	tcg	ttc	720	
Met	Pro	Val	Tyr	Leu	Thr	Phe	Asp	Ile	Asp	Cys	Leu	Asp	Pro	Ser	Phe		
					230					235					240		
gcc	ccc	ggg	acc	ggg	acg	ccc	gta	tgc	ggc	ggc	ttg	agc	agc	gac	agg	768	
Ala	Pro	Gly	Thr	Gly	Thr	Pro	Val	Cys	Gly	Gly	Leu	Ser	Ser	Asp	Arg		
				245					250					255			
gca	tta	aaa	atc	cta	cgt	ggg	ctg	acg	gat	ctc	gac	atc	gtc	ggg	atg	816	
Ala	Leu	Lys	Ile	Leu	Arg	Gly	Leu	Thr	Asp	Leu	Asp	Ile	Val	Gly	Met		
			260					265					270				
gat	gtt	gta	gaa	gtt	gcc	ccc	tct	tac	gac	caa	tcc	gac	att	acc	gct	864	
Asp	Val	Val	Glu	Val	Ala	Pro	Ser	Tyr	Asp	Gln	Ser	Asp	Ile	Thr	Ala		
		275					280					285					
ttg	gcc	ggc	gcc	aca	att	gcc	ttg	gaa	atg	ctt	tac	ctt	caa	ggg	gcg	912	
Leu	Ala	Gly	Ala	Thr	Ile	Ala	Leu	Glu	Met	Leu	Tyr	Leu	Gln	Gly	Ala		
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aaa	aag	gac	tga													924	
Lys	Lys	Asp															
		305															

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 <213> Neisseria meningitidis

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 20 25 30  
 Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val  
 35 40 45  
 Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala  
 50 55 60  
 Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp  
 65 70 75 80  
 Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser  
 85 90 95

093043-081601

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<222> (1) .. (423)
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1 5 10 15

att ccc tac ccc gtc acc agg cgg att gcc tca agt ttg tat tcc acc 96  
Ile Pro Tyr Pro Val Thr Arg Arg Ile Ala Ser Ser Leu Tyr Ser Thr  
20 25 30

gaa tat ttt gtc gta tgc ttt ctg cgt ttg atg cca ctc tct ccg tgt 144  
Glu Tyr Phe Val Val Cys Phe Leu Arg Leu Met Pro Leu Ser Pro Cys  
35 40 45

aat ctg tat ttt gtc acc cat ctg cgt acc aat gaa tcc gaa ata gaa 192  
Asn Leu Tyr Phe Val Thr His Leu Arg Thr Asn Glu Ser Glu Ile Glu  
50 55 60

aga tgg tct gct gtt ccc tgc caa ata gta ttg aac gac ggc aag tcc 240  
Arg Trp Ser Ala Val Pro Cys Gln Ile Val Leu Asn Asp Gly Lys Ser  
65 70 75 80

gaa ttc ggc gga ttc gca ttt gaa gtg caa ctt tcc cta aca gaa aaa 288  
Glu Phe Gly Gly Phe Ala Phe Glu Val Gln Leu Ser Leu Thr Glu Lys  
85 90 95

ggc cag tat gcg gta gca tac gac ctt tcc tgc aag aaa gat tgc cat 336  
Gly Gln Tyr Ala Val Ala Tyr Asp Leu Ser Cys Lys Lys Asp Cys His  
100 105 110

gag cta cac gca act gac cca agg cga acg ata cca cat cca ata cct 384  
Glu Leu His Ala Thr Asp Pro Arg Arg Thr Ile Pro His Pro Ile Pro  
115 120 125

gtc ccg cca ctg cac cgt cac cga aat cgc caa aca gct taa 426  
Val Pro Pro Leu His Arg His Arg Asn Arg Gln Thr Ala  
130 135 140

<210> 26  
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<212> PRT  
<213> Neisseria meningitidis

09830433-081604

<400> 26

Met Glu Gln Ser Gly Lys Phe Ser Trp Ser Ala Ala Ala Phe Trp Asp  
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Ile Pro Tyr Pro Val Thr Arg Arg Ile Ala Ser Ser Leu Tyr Ser Thr  
20 25 30

Glu Tyr Phe Val Val Cys Phe Leu Arg Leu Met Pro Leu Ser Pro Cys  
35 40 45

Asn Leu Tyr Phe Val Thr His Leu Arg Thr Asn Glu Ser Glu Ile Glu  
50 55 60

Arg Trp Ser Ala Val Pro Cys Gln Ile Val Leu Asn Asp Gly Lys Ser  
65 70 75 80

Glu Phe Gly Gly Phe Ala Phe Glu Val Gln Leu Ser Leu Thr Glu Lys  
85 90 95

Gly Gln Tyr Ala Val Ala Tyr Asp Leu Ser Cys Lys Lys Asp Cys His  
100 105 110

Glu Leu His Ala Thr Asp Pro Arg Arg Thr Ile Pro His Pro Ile Pro  
115 120 125

Val Pro Pro Leu His Arg His Arg Asn Arg Gln Thr Ala  
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<211> 351

<212> DNA

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ggg att atg ctg ttg aag gta gta cct gag cgt acc gtt tcg gca gat 96  
Gly Ile Met Leu Lys Val Val Pro Glu Arg Thr Val Ser Ala Asp  
20 25 30

gca aaa acc aga gac ccg atg tgg gac aat gcg gct tta cag acc agc 144  
Ala Lys Thr Arg Asp Pro Met Trp Asp Asn Ala Ala Leu Gln Thr Ser  
35 40 45

gaa ggc gta aat ttt att gct cgt ttc cta gga ttt ttt agc gat ggg 192  
Glu Gly Val Asn Phe Ile Ala Arg Phe Leu Gly Phe Phe Ser Asp Gly  
50 55 60

gaa tac cgc tat gtg gat gtc ctg caa ccc aac cat tcc gat att att 240  
Glu Tyr Arg Tyr Val Asp Val Leu Gln Pro Asn His Ser Asp Ile Ile  
65 70 75 80

cgg tat tca ggt aaa gat ttt ccg cta aat caa ata ctt aac cat ata 288  
Arg Tyr Ser Gly Lys Asp Phe Pro Leu Asn Gln Ile Leu Asn His Ile  
85 90 95

cac ccc gcc cgt tat gcg gta acg ttc gaa aac aat gtc gat tcc aag 336  
His Pro Ala Arg Tyr Ala Val Thr Phe Glu Asn Asn Val Asp Ser Lys  
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ctg cgc agg cac tga 351  
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<210> 28

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<212> PRT

<213> Neisseria meningitidis

<400> 28

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Gly Ile Met Leu Lys Val Val Pro Glu Arg Thr Val Ser Ala Asp  
20 25 30

0903043-031601

Ala Lys Thr Arg Asp Pro Met Trp Asp Asn Ala Ala Leu Gln Thr Ser  
 35 40 45  
 Glu Gly Val Asn Phe Ile Ala Arg Phe Leu Gly Phe Phe Ser Asp Gly  
 50 55 60  
 Glu Tyr Arg Tyr Val Asp Val Leu Gln Pro Asn His Ser Asp Ile Ile  
 65 70 75 80  
 Arg Tyr Ser Gly Lys Asp Phe Pro Leu Asn Gln Ile Leu Asn His Ile  
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 His Pro Ala Arg Tyr Ala Val Thr Phe Glu Asn Asn Val Asp Ser Lys  
 100 105 110  
 Leu Arg Arg His  
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 1 5 10 15  
 tgc ctg aca ctg acg ccc tat ttg caa cat gaa cta ttt tcg gct atg 96  
 Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met  
 20 25 30  
 aaa tcc tat ttt tcc aaa tat atc cta ccc gtt tca ctt ttt acc ttg 144  
 Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu  
 35 40 45  
 cca cta tcc ctt tcc cca tcc gtt tcg gct ttt acg ctg cct gaa gca 192  
 Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala  
 50 55 60  
 tgg cgg gcg gcg cag caa cat tcg gct gat ttt caa gcg tcc cat tac 240  
 Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr  
 65 70 75 80  
 cag cgt gat gca gtg cgc gca cgg caa caa caa gcc aag gcc gca ttc 288  
 Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe  
 85 90 95  
 ctt ccc cat gta tcc gcc aat gcc agc tac cag cgc cag ccg cca tcg 336  
 Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser  
 100 105 110  
 att tct tcc acc cgc gaa aca cag gga tgg agc gtg cag gtg gga caa 384

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Ile	Ser	Thr	Arg	Glu	Thr	Gln	Gly	Trp	Ser	Val	Gln	Val	Gly	Gln		
	115					120					125					
acc	tta	ttt	gac	gct	gcc	aaa	ttt	gca	caa	tac	cgc	caa	agc	agg	ttc	432
Thr	Leu	Phe	Asp	Ala	Ala	Lys	Phe	Ala	Gln	Tyr	Arg	Gln	Ser	Arg	Phe	
	130					135					140					
gat	acg	cag	gct	gca	gaa	cag	cgt	ttc	gat	gcg	gca	cgc	gaa	gaa	ttg	480
Asp	Thr	Gln	Ala	Ala	Glu	Gln	Arg	Phe	Asp	Ala	Ala	Arg	Glu	Glu	Leu	
	145				150					155					160	
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Leu	Leu	Lys	Val	Ala	Glu	Ser	Tyr	Phe	Asn	Val	Leu	Leu	Ser	Arg	Asp	
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Thr	Val	Ala	Ala	His	Ala	Ala	Glu	Lys	Glu	Ala	Tyr	Ala	Gln	Gln	Val	
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agg	cag	gcg	cag	gct	tta	ttc	aat	aaa	ggc	gct	gcc	acc	gcg	ctg	gat	624
Arg	Gln	Ala	Gln	Ala	Leu	Phe	Asn	Lys	Gly	Ala	Ala	Thr	Ala	Leu	Asp	
		195					200					205				
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Ile	His	Glu	Ala	Lys	Ala	Gly	Tyr	Asp	Asn	Ala	Leu	Ala	Gln	Glu	Ile	
						215					220					
gcc	gta	ttg	gct	gag	aaa	caa	acc	tat	gaa	aac	cag	ttg	aac	gac	tac	720
Ala	Val	Leu	Ala	Glu	Lys	Gln	Thr	Tyr	Glu	Asn	Gln	Leu	Asn	Asp	Tyr	
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acc	gac	ctg	gat	agc	aaa	caa	atc	gag	gcc	ata	gat	acc	gcc	aac	ctg	768
Thr	Asp	Leu	Asp	Ser	Lys	Gln	Ile	Glu	Ala	Ile	Asp	Thr	Ala	Asn	Leu	
				245					250					255		
ttg	gca	cgc	tat	ctg	ccc	aag	ctg	gaa	cgt	tac	agt	ctg	gat	gaa	tgg	816
Leu	Ala	Arg	Tyr	Leu	Pro	Lys	Leu	Glu	Arg	Tyr	Ser	Leu	Asp	Glu	Trp	
				260				265					270			
cag	cgc	att	gcc	tta	tcc	aac	aat	cat	gaa	tac	cgg	atg	cag	cag	ctt	864
Gln	Arg	Ile	Ala	Leu	Ser	Asn	Asn	His	Glu	Tyr	Arg	Met	Gln	Gln	Leu	
		275					280					285				
gcc	ctg	caa	agc	agc	gga	cag	gcg	ctt	cgg	gca	gca	cag	aac	agc	cgc	912
Ala	Leu	Gln	Ser	Ser	Gly	Gln	Ala	Leu	Arg	Ala	Ala	Gln	Asn	Ser	Arg	
						295				300						
tat	ccc	acc	gtt	tct	gcc	cat	gtc	ggc	tat	cag	aat	aac	ctc	tac	act	960
Tyr	Pro	Thr	Val	Ser	Ala	His	Val	Gly	Tyr	Gln	Asn	Asn	Leu	Tyr	Thr	
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tca	tct	gcg	cag	aat	aat	gac	tac	cac	tat	cgg	ggc	aaa	ggg	atg	agc	1008

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln  
 355 360 365

ctg acc gca acc gag cgg cac atc aaa ctc gcc gta cgc cag gct tat 1152  
 Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr  
 370 375 380

acc gaa agc ggt gcg gcg cgt tac caa atc atg gcg caa gaa cgg gtt 1200  
 Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val  
 385 390 395 400

ttg gaa agc agc cgt ttg aaa ctg aaa tgc acc gaa acc ggc caa caa 1248  
 Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln  
 405 410 415

tac ggc atc cgc aac cgg ctg gaa gta ata cgg gcg cgg cag gaa gtc 1296  
 Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val  
 420 425 430

gcc caa gca gaa cag aaa ctg gct caa gca cgg tat aaa ttc atg ctg 1344  
 Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu  
 435 440 445

gct tat ttg cgc ttg gtg aaa gag agc ggg tta ggg ttg gaa atg gta 1392  
 Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val  
 450 455 460

ttt gcg gaa taa 1404  
 Phe Ala Glu  
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 <213> Neisseria meningitidis

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Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu  
 35 40 45

Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala  
 50 55 60

Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr  
 65 70 75 80

Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe  
 85 90 95

Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser  
 100 105 110

Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln

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115	120	125
Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe 130 135 140		
Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu 145 150 155 160		
Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp 165 170 175		
Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val 180 185 190		
Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp 195 200 205		
Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile 210 215 220		
Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr 225 230 235 240		
Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu 245 250 255		
Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp 260 265 270		
Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu 275 280 285		
Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg 290 295 300		
Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr 305 310 315 320		
Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser 325 330 335		
Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser 340 345 350		
Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln 355 360 365		
Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr 370 375 380		
Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val 385 390 395 400		
Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln 405 410 415		
Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val 420 425 430		
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0980433-08160

445

[illegible]

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 165 170 175

gat aaa gat ttg cga gaa cct gat gcc ggc ctg ttg ttg aat att ttc 576  
 Asp Lys Asp Leu Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe  
 180 185 190

gac ctg tat tac gat ttg gct tcc gcg ccg gca cca ata tgt cgc caa 624  
 Asp Leu Tyr Tyr Asp Leu Ala Ser Ala Pro Ala Pro Ile Cys Arg Gln  
 195 200 205

gcg cgc cca cat ttt gga agc agc aaa aaa agc gtc aac atg gca tat 672  
 Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr  
 210 215 220

ccg tca tgt tgc gcc caa gta taa 696  
 Pro Ser Cys Cys Ala Gln Val  
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Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile  
 20 25 30

Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala  
 35 40 45

Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly  
 50 55 60

Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr  
 65 70 75 80

Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln  
 85 90 95

Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe  
 100 105 110

Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe  
 115 120 125

Ile Phe Gly Leu Thr Val Trp Arg Tyr Cys Val Ser Gly Gly Val Phe  
 130 135 140

Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile  
 145 150 155 160

Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Asp Lys Ile Ala Ser  
 165 170 175

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Asp Lys Asp Leu Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe  
 180 185 190  
 Asp Leu Tyr Tyr Asp Leu Ala Ser Ala Pro Ala Pro Ile Cys Arg Gln  
 195 200 205  
 Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr  
 210 215 220  
 Pro Ser Cys Cys Ala Gln Val  
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 <212> DNA  
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 acc aaa ggg ctg ttg ata aac ggt tac cat ttc acc gcc cac gcg acg 96  
 Thr Lys Gly Leu Leu Ile Asn Gly Tyr His Phe Thr Ala His Ala Thr  
 20 25 30  
 aat ctt tgg ctg ccg cag act ttg ggg ctg ccg gga gag ccg aac aat 144  
 Asn Leu Ser Leu Pro Gln Thr Leu Gly Leu Pro Gly Glu Pro Asn Asn  
 35 40 45  
 aac att gtc agc ttg gcc aag cag gcg ggt ttt cgg acg gcg tgg ctg 192  
 Asn Ile Val Ser Leu Ala Lys Gln Ala Gly Phe Arg Thr Ala Trp Leu  
 50 55 60  
 tct aat caa gga atg ttg ggg cat ttt gcc aac gaa att tcc acc tat 240  
 Ser Asn Gln Gly Met Leu Gly His Phe Ala Asn Glu Ile Ser Thr Tyr  
 65 70 75 80  
 gcc cta cgc agc gat tat ccg tgg ttt acc caa agg ggt gat tat gcc 288  
 Ala Leu Arg Ser Asp Tyr Pro Trp Phe Thr Gln Arg Gly Asp Tyr Gly  
 85 90 95  
 aaa agc gcg ggg ttg agc gac cgc ctt ttg ttg ccg gcg ttc aaa cgg 336  
 Lys Ser Ala Gly Leu Ser Asp Arg Leu Leu Leu Pro Ala Phe Lys Arg  
 100 105 110  
 gtt ttg ata gga aat gca ggc acg aag cct cgg ctg att gtg atg cac 384  
 Val Leu Ile Gly Asn Ala Gly Thr Lys Pro Arg Leu Ile Val Met His  
 115 120 125  
 ctg atg ggt tgg cac agt gat ttt tgc aca cgt ttg gat aag gat gcc 432  
 Leu Met Gly Ser His Ser Asp Phe Cys Thr Arg Leu Asp Lys Asp Ala  
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Thr	Lys	Gly	Leu	Leu	Ile	Asn	Gly	Tyr	His	Phe	Thr	Ala	His	Ala	Thr
			20					25					30		
Asn	Leu	Ser	Leu	Pro	Gln	Thr	Leu	Gly	Leu	Pro	Gly	Glu	Pro	Asn	Asn
		35					40					45			
Asn	Ile	Val	Ser	Leu	Ala	Lys	Gln	Ala	Gly	Phe	Arg	Thr	Ala	Trp	Leu
	50					55					60				
Ser	Asn	Gln	Gly	Met	Leu	Gly	His	Phe	Ala	Asn	Glu	Ile	Ser	Thr	Tyr

65		70		75		80									
Ala	Leu	Arg	Ser	Asp	Tyr	Pro	Trp	Phe	Thr	Gln	Arg	Gly	Asp	Tyr	Gly
				85					90					95	
Lys	Ser	Ala	Gly	Leu	Ser	Asp	Arg	Leu	Leu	Leu	Pro	Ala	Phe	Lys	Arg
			100					105					110		
Val	Leu	Ile	Gly	Asn	Ala	Gly	Thr	Lys	Pro	Arg	Leu	Ile	Val	Met	His
		115					120					125			
Leu	Met	Gly	Ser	His	Ser	Asp	Phe	Cys	Thr	Arg	Leu	Asp	Lys	Asp	Ala
	130					135					140				
Arg	Arg	Phe	Gln	Tyr	Gln	Thr	Glu	Lys	Ile	Ser	Cys	Tyr	Val	Ser	Thr
145					150					155					160
Ile	Ala	Gln	Thr	Asp	Lys	Phe	Leu	Glu	Asp	Thr	Val	Lys	Ile	Leu	Asn
				165					170					175	
Glu	Asn	Lys	Glu	Ser	Trp	Ser	Leu	Val	Tyr	Phe	Ser	Asp	His	Gly	Leu
			180					185					190		
Met	His	Val	Gly	Lys	Gly	Gly	Glu	Arg	Thr	Leu	Thr	His	Gly	Ala	Trp
	195						200					205			
Lys	Arg	Gln	Ser	Tyr	Gly	Val	Pro	Leu	Val	Lys	Ile	Ser	Ser	Asp	Asp
	210					215					220				
Thr	Arg	Arg	Glu	Met	Ile	Lys	Val	Arg	Arg	Ser	Ala	Phe	Asn	Phe	Leu
225					230					235					240
Arg	Gly	Phe	Gly	Ser	Trp	Thr	Gly	Ile	Glu	Thr	Asp	Glu	Leu	Pro	Asp
				245				250					255		
Asp	Gly	Tyr	Asp	Phe	Trp	Gly	Asn	Val	Pro	Asp	Val	Gln	Gly	Glu	Gly
			260				265						270		
Asn	Asn	Leu	Ala	Phe	Ile	Asp	Gly	Leu	Pro	Asp	Asp	Pro	Ala	Pro	Trp
	275						280					285			
Tyr	Ala	Gly	Lys	Gly	Lys	Ser	Thr	Lys	Asn	Thr	Ser	Lys	Lys		
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gaa tcg aat ccg ctt gcc gtc gcc ggt tgc gtc aat gct tat ttt gca 96  
Glu Ser Asn Pro Leu Ala Val Ala Gly Cys Val Asn Ala Tyr Phe Ala  
20 25 30

cga ttg gcc acc caa agc ggt ttc aaa gcc atc tat ctg tcc ggc ggc 144  
Arg Leu Ala Thr Gln Ser Gly Phe Lys Ala Ile Tyr Leu Ser Gly Gly  
35 40 45

ggc gtg gca gcc tgt tct tgc ggt atc cct gat ttg ggc att acc aca 192  
Gly Val Ala Ala Cys Ser Cys Gly Ile Pro Asp Leu Gly Ile Thr Thr  
50 55 60

atg gaa gat gtg ctg atc gac gca cga cgc att acg gac aac gtg gat 240  
Met Glu Asp Val Leu Ile Asp Ala Arg Arg Ile Thr Asp Asn Val Asp  
65 70 75 80

acg cct ctg ctg gtg gac atc gat gtg ggt tgg ggc ggt gca ttc aat 288  
Thr Pro Leu Leu Val Asp Ile Asp Val Gly Trp Gly Gly Ala Phe Asn  
85 90 95

att gcc cgt acc att cgc aac ttt gaa cgc gcc ggt gtt gca gcg gtt 336  
Ile Ala Arg Thr Ile Arg Asn Phe Glu Arg Ala Gly Val Ala Ala Val  
100 105 110

cac atc gaa gat cag gta ggc caa aaa cgc tgc ggc cac cgt ccg aac 384  
His Ile Glu Asp Gln Val Ala Gln Lys Arg Cys Gly His Arg Pro Asn  
115 120 125

aaa gcc att gta tct aaa gat gaa atg gtc gac cgt atc aaa gct gcc 432  
Lys Ala Ile Val Ser Lys Asp Glu Met Val Asp Arg Ile Lys Ala Ala  
130 135 140

gta gat gcg cgc gtt gat gag aac ttc gtc att atg gcg cgt acc gat 480  
Val Asp Ala Arg Val Asp Glu Asn Phe Val Ile Met Ala Arg Thr Asp  
145 150 155 160

gcg ctg gcg gta gaa ggt tgg gat gcc gct atc gaa cgt gcc caa gct 528  
Ala Leu Ala Val Glu Gly Leu Asp Ala Ile Glu Arg Ala Gln Ala  
165 170 175

tgt gtc gaa gcc ggt gcg gac atg att ttc cct gaa gcc atg acc gat 576  
Cys Val Glu Ala Gly Ala Asp Met Ile Phe Pro Gly Ala Met Thr Asp  
180 185 190

ttg aac atg tac cgc caa ttt gca gat gcg gtc aaa gtc ccc gtg ttg 624  
Leu Asn Met Tyr Arg Gln Phe Ala Asp Ala Val Lys Val Pro Val Leu  
195 200 205

ggc aac att acc gag ttt ggt tcc acc ccg ctt tat acc caa agc gag 672  
Ala Asn Ile Thr Glu Phe Gly Ser Thr Pro Leu Tyr Thr Gln Ser Glu  
210 215 220

ctg gct gaa aac ggc gtg tgg ctg gtc ctg tat ccg ctg tca tcc ttc 720  
Leu Ala Glu Asn Gly Val Ser Leu Val Leu Tyr Pro Leu Ser Ser Phe  
225 230 235 240

cgt gca gca agc aaa gcc gct ctg aat gtt tac gaa gcg att atg cgc 768  
Arg Ala Ala Ser Lys Ala Ala Leu Asn Val Tyr Glu Ala Ile Met Arg  
245 250 255

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gat ggc act tca ggc ggc ggt ggt gga cag tat gca aac ccg tgc cga 816  
Asp Gly Thr Ser Gly Gly Gly Gly Gln Tyr Ala Asn Pro Cys Arg  
260 265 270

gct gta cga gca tct gaa cta tca tgc ctt cga gca aaa act gga taa 864  
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<213> Neisseria meningitidis

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35 40 45  
Gly Val Ala Ala Cys Ser Cys Gly Ile Pro Asp Leu Gly Ile Thr Thr  
50 55 60  
Met Glu Asp Val Leu Ile Asp Ala Arg Arg Ile Thr Asp Asn Val Asp  
65 70 75 80  
Thr Pro Leu Leu Val Asp Ile Asp Val Gly Trp Gly Gly Ala Phe Asn  
85 90 95  
Ile Ala Arg Thr Ile Arg Asn Phe Glu Arg Ala Gly Val Ala Ala Val  
100 105 110  
His Ile Glu Asp Gln Val Ala Gln Lys Arg Cys Gly His Arg Pro Asn  
115 120 125  
Lys Ala Ile Val Ser Lys Asp Glu Met Val Asp Arg Ile Lys Ala Ala  
130 135 140  
Val Asp Ala Arg Val Asp Glu Asn Phe Val Ile Met Ala Arg Thr Asp  
145 150 155 160  
Ala Leu Ala Val Glu Gly Leu Asp Ala Ala Ile Glu Arg Ala Gln Ala  
165 170 175  
Cys Val Glu Ala Gly Ala Asp Met Ile Phe Pro Glu Ala Met Thr Asp  
180 185 190  
Leu Asn Met Tyr Arg Gln Phe Ala Asp Ala Val Lys Val Pro Val Leu  
195 200 205  
Ala Asn Ile Thr Glu Phe Gly Ser Thr Pro Leu Tyr Thr Gln Ser Glu  
210 215 220  
Leu Ala Glu Asn Gly Val Ser Leu Val Leu Tyr Pro Leu Ser Ser Phe  
225 230 235 240

109180" EETH0E960

Arg Ala Ala Ser Lys Ala Ala Leu Asn Val Tyr Glu Ala Ile Met Arg  
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 260 265 270  
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 275 280 285

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 5 10 15  
 ctt tca gac tgc ctt tca aca aat ccg cat cgg tgg tct gaa aac ccg 96  
 Leu Ser Asp Cys Leu Ser Thr Asn Pro His Arg Ser Ser Glu Asn Pro  
 20 25 30  
 aaa ccc ata aaa aca caa agg aga aat acc atg act gaa act acc caa 144  
 Lys Pro Ile Lys Thr Gln Arg Arg Asn Thr Met Thr Glu Thr Thr Gln  
 35 40 45  
 acc ccg acc ctc aaa cct aaa aaa tcc ggt gcg ctt tct ggc gtt gcg 192  
 Thr Pro Thr Leu Lys Pro Lys Lys Ser Val Ala Leu Ser Gly Val Ala  
 50 55 60  
 gcc ggt aat acc gct ttg tgt acc gtt ggc cgt acc ggc aac gat ttg 240  
 Ala Gly Asn Thr Ala Leu Cys Thr Val Gly Arg Thr Gly Asn Asp Leu  
 65 70 75 80  
 agc tat cgc ggt tac gac att ctg gat ttg gca caa aaa tgt gag ttt 288  
 Ser Tyr Arg Gly Tyr Asp Ile Leu Asp Leu Ala Gln Lys Cys Glu Phe  
 85 90 95  
 gaa gaa gtt gcc cac ctg ctg att cac ggc cat tta ccc aac aaa ttc 336  
 Glu Glu Val Ala His Leu Leu Ile His Gly His Leu Pro Asn Lys Phe  
 100 105 110  
 gag ctg gcc gct tat aaa gcc aag ctt aaa tcc atg cgc ggc ctg cct 384  
 Glu Leu Ala Ala Tyr Lys Ala Lys Leu Lys Ser Met Arg Gly Leu Pro  
 115 120 125  
 atc cgt gtg att aaa gtt ttg gaa agc ctg cct gca cat acc cat ccg 432  
 Ile Arg Val Ile Lys Val Leu Glu Ser Leu Pro Ala His Thr His Pro  
 130 135 140  
 atg gac gtg atg cgt acc ggc gta tcc atg ctg ggc tgt gtt cat cct 480  
 Met Asp Val Met Arg Thr Gly Val Ser Met Leu Gly Cys Val His Pro  
 145 150 155 160

093043-081601

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<210> 38
<211> 306
<212> PRT
<213> Neisseria meningitidis
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Met	Pro	Ser	Ser	Lys	Asn	Trp	Ile	Asn	Cys	Phe	Lys	Asn	Asp	Leu	Pro
1				5					10					15	
Leu	Ser	Asp	Cys	Leu	Ser	Thr	Asn	Pro	His	Arg	Ser	Ser	Glu	Asn	Pro
			20					25					30		
Lys	Pro	Ile	Lys	Thr	Gln	Arg	Arg	Asn	Thr	Met	Thr	Glu	Thr	Thr	Gln
		35					40					45			
Thr	Pro	Thr	Leu	Lys	Pro	Lys	Lys	Ser	Val	Ala	Leu	Ser	Gly	Val	Ala
	50					55					60				

Ala	Gly	Asn	Thr	Ala	Leu	Cys	Thr	Val	Gly	Arg	Thr	Gly	Asn	Asp	Leu	65	70	75	80
Ser	Tyr	Arg	Gly	Tyr	Asp	Ile	Leu	Asp	Leu	Ala	Gln	Lys	Cys	Glu	Phe	85	90	95	
Glu	Glu	Val	Ala	His	Leu	Leu	Ile	His	Gly	His	Leu	Pro	Asn	Lys	Phe	100	105	110	
Glu	Leu	Ala	Ala	Tyr	Lys	Ala	Lys	Leu	Lys	Ser	Met	Arg	Gly	Leu	Pro	115	120	125	
Ile	Arg	Val	Ile	Lys	Val	Leu	Glu	Ser	Leu	Pro	Ala	His	Thr	His	Pro	130	135	140	
Met	Asp	Val	Met	Arg	Thr	Gly	Val	Ser	Met	Leu	Gly	Cys	Val	His	Pro	145	150	155	160
Glu	Arg	Glu	Gly	His	Pro	Glu	Ser	Glu	Ala	Arg	Asp	Ile	Ala	Asp	Lys	165	170	175	
Leu	Ile	Ala	Ser	Leu	Gly	Ser	Ile	Leu	Leu	Tyr	Trp	Tyr	Gln	Tyr	Ser	180	185	190	
His	Asn	Gly	Lys	Arg	Ile	Glu	Val	Glu	Ser	Glu	Glu	Glu	Thr	Ile	Gly	195	200	205	
Gly	His	Phe	Leu	His	Leu	Leu	His	Gly	Lys	Arg	Pro	Ser	Glu	Ser	His	210	215	220	
Ile	Lys	Ala	Met	His	Val	Ser	Leu	Ile	Leu	Tyr	Ala	Glu	His	Glu	Phe	225	230	235	240
Asn	Ala	Ser	Thr	Phe	Thr	Ala	Arg	Val	Ile	Ala	Gly	Thr	Gly	Ser	Asp	245	250	255	
Met	Tyr	Ser	Ser	Ile	Thr	Gly	Ala	Ile	Gly	Ala	Leu	Lys	Gly	Pro	Lys	260	265	270	
His	Gly	Gly	Ala	Asn	Glu	Gly	Leu	Thr	Ile	Phe	Lys	Asn	Ala	Thr	Ala	275	280	285	
Met	Pro	Thr	Lys	Pro	Lys	Pro	Thr	Ser	Ala	Asn	Ala	Ser	Ala	Ala	Lys	290	295	300	
Lys	Ser															305			

<210> 39  
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 <212> DNA  
 <213> Neisseria meningitidis

<220>  
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09030433-031601

<400> 39

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Met His Leu Cys Gly Lys Tyr Tyr Gly Val Asn Met Lys Leu Arg Asp	
1 5 10 15	
tta ctg atg gga ata ttc ttg gca gtt tct gcg gcc ctt ctg aat gca	96
Leu Leu Met Gly Ile Phe Leu Ala Val Ser Ala Ala Leu Leu Asn Ala	
20 25 30	
acc atc ggc ata ttc agc aag ata ttg atg gag cag ggc ttg tct gtt	144
Thr Ile Gly Ile Phe Ser Lys Ile Leu Met Glu Gln Gly Leu Ser Val	
35 40 45	
cag cat att gca ttt ttg aaa act ttg aca ggt ttc gtg ttt atc agc	192
Gln His Ile Ala Phe Leu Lys Thr Leu Thr Gly Phe Val Phe Ile Ser	
50 55 60	
att ttg ctt tgc cgt acc ggt ttt acc aga cag att gcg gat att tca	240
Ile Leu Leu Cys Arg Thr Gly Phe Thr Arg Gln Ile Ala Asp Ile Ser	
65 70 75 80	
aga aag aaa gag gca att ttg ccg ttg ctg tta aaa gta gca att tgt	288
Arg Lys Lys Glu Ala Ile Leu Pro Leu Leu Leu Lys Val Ala Ile Cys	
85 90 95	
gct ttt ttc gga att tat acg ttg ttt ttc ttt gaa acc aca gct tat	336
Ala Phe Phe Gly Ile Tyr Thr Leu Phe Phe Phe Glu Thr Thr Ala Tyr	
100 105 110	
caa tat ggc aat gct gcg aat gta gta gtt gta tta atg gca tcg gct	384
Gln Tyr Gly Asn Ala Ala Asn Val Val Val Val Leu Met Ala Ser Ala	
115 120 125	
gcc gta tct gcc ttg ata ttg gac agc ata ctg tta gat gaa cgt att	432
Ala Val Ser Ala Leu Ile Leu Asp Ser Ile Leu Leu Asp Glu Arg Ile	
130 135 140	
tgc att tct tca gtc gtc ggt gtg ggt ttg gca gta ttg ggg atc gca	480
Cys Ile Ser Ser Val Val Gly Val Gly Leu Ala Val Leu Gly Ile Ala	
145 150 155 160	
atg att tct tgg act gga gaa gga agt tta ggg ttg att ctg aat gcc	528
Met Ile Ser Trp Thr Gly Glu Gly Ser Leu Gly Leu Ile Leu Asn Ala	
165 170 175	
gca ctg gcg ggc tcg ggc tac ggt tgt ttt tcc gtt ttg att aag aaa	576
Ala Leu Ala Gly Ser Gly Tyr Gly Cys Phe Ser Val Leu Ile Lys Lys	
180 185 190	
ttc ggc cta aac ggc ggt att tat ttg aca cgg ata ttg atg ttt ttt	624
Phe Gly Leu Asn Gly Gly Ile Tyr Leu Thr Arg Ile Leu Met Phe Phe	
195 200 205	
gga agt att ttt ttg ttt atc cct tca ttg gaa ggt att gag gat ata	672
Gly Ser Ile Phe Leu Phe Ile Pro Ser Leu Glu Gly Ile Glu Asp Ile	
210 215 220	
cat tgg caa tgg tct ttt att ccg cca ctc ttg gca ttg tct tta ttg	720
His Trp Gln Trp Ser Phe Ile Pro Pro Leu Leu Ala Leu Ser Leu Leu	
225 230 235 240	

09830433 081604

ccg acg att tta gga ttt tat tgt aca act aaa gca ttg gat tat ttg	768
Pro Thr Ile Leu Gly Phe Tyr Cys Thr Thr Lys Ala Leu Asp Tyr Leu	
245 250 255	
agt gct gcg aag gta cag gta act gaa ttg gcc gag cca ttg ttt gct	816
Ser Ala Ala Lys Val Gln Val Thr Glu Leu Ala Glu Pro Leu Phe Ala	
260 265 270	
gcc gta ctg gct tgg ttg ttt ttg aat gaa ata ccg gaa gga cgc ttc	864
Ala Val Leu Ala Trp Leu Phe Leu Asn Glu Ile Pro Glu Gly Arg Phe	
275 280 285	
ttt gtc ggc gcc att ctg att att gcc ggt att gtg tct atc aat ggg	912
Phe Val Gly Ala Ile Leu Ile Ile Ala Gly Ile Val Ser Ile Asn Gly	
290 295 300	
ctg tat cga cca ttg ttg aag cga att gaa taa	945
Leu Tyr Arg Pro Leu Leu Lys Arg Ile Glu	
305 310	

<210> 40  
 <211> 314  
 <212> PRT  
 <213> Neisseria meningitidis

<400> 40

Met His Leu Cys Gly Lys Tyr Tyr Gly Val Asn Met Lys Leu Arg Asp	
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Leu Leu Met Gly Ile Phe Leu Ala Val Ser Ala Ala Leu Leu Asn Ala	
20 25 30	
Thr Ile Gly Ile Phe Ser Lys Ile Leu Met Glu Gln Gly Leu Ser Val	
35 40 45	
Gln His Ile Ala Phe Leu Lys Thr Leu Thr Gly Phe Val Phe Ile Ser	
50 55 60	
Ile Leu Leu Cys Arg Thr Gly Phe Thr Arg Gln Ile Ala Asp Ile Ser	
65 70 75 80	
Arg Lys Lys Glu Ala Ile Leu Pro Leu Leu Lys Val Ala Ile Cys	
85 90 95	
Ala Phe Phe Gly Ile Tyr Thr Leu Phe Phe Phe Glu Thr Thr Ala Tyr	
100 105 110	
Gln Tyr Gly Asn Ala Ala Asn Val Val Val Val Leu Met Ala Ser Ala	
115 120 125	
Ala Val Ser Ala Leu Ile Leu Asp Ser Ile Leu Leu Asp Glu Arg Ile	
130 135 140	
Cys Ile Ser Ser Val Val Gly Val Gly Leu Ala Val Leu Gly Ile Ala	
145 150 155 160	
Met Ile Ser Trp Thr Gly Glu Gly Ser Leu Gly Leu Ile Leu Asn Ala	
165 170 175	

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Ala Leu Ala Gly Ser Gly Tyr Gly Cys Phe Ser Val Leu Ile Lys Lys  
180 185 190

Phe Gly Leu Asn Gly Gly Ile Tyr Leu Thr Arg Ile Leu Met Phe Phe  
195 200 205

Gly Ser Ile Phe Leu Phe Ile Pro Ser Leu Glu Gly Ile Glu Asp Ile  
210 215 220

His Trp Gln Trp Ser Phe Ile Pro Pro Leu Leu Ala Leu Ser Leu Leu  
225 230 235 240

Pro Thr Ile Leu Gly Phe Tyr Cys Thr Thr Lys Ala Leu Asp Tyr Leu  
245 250 255

Ser Ala Ala Lys Val Gln Val Thr Glu Leu Ala Glu Pro Leu Phe Ala  
260 265 270

Ala Val Leu Ala Trp Leu Phe Leu Asn Glu Ile Pro Glu Gly Arg Phe  
275 280 285

Phe Val Gly Ala Ile Leu Ile Ile Ala Gly Ile Val Ser Ile Asn Gly  
290 295 300

Leu Tyr Arg Pro Leu Leu Lys Arg Ile Glu  
305 310

<210> 41  
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<212> DNA  
<213> Neisseria meningitidis

<220>  
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gaa tac tac gac gcg cgt gcg gcg tgt gag gac atc aag ccc ggc tct 96  
Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Asp Ile Lys Pro Gly Ser  
20 25 30

tac gac aag ctg cct tac acg agc cgc att ttg gcg gag aat ttg gtc 144  
Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val  
35 40 45

aac cgc gcg gac aaa gtc gat ttg ccg acg ctg caa agc tgg ctg ggt 192  
Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly  
50 55 60

cag ctg att gag gga aaa cag gaa atc gac ttt cct tgg tat ccg gcg 240  
Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala  
65 70 75 80

cgg gtg gtg tgc cac gat att ctg ggg cag acc gcg ttg gtg gat ttg 288

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Arg	Val	Val	Cys	His	Asp	Ile	Leu	Gly	Gln	Thr	Ala	Leu	Val	Asp	Leu			
85																90		
95																		
gca	ggt	ctg	cgc	gat	gcg	att	gcc	gaa	aaa	ggc	ggc	gat	cct	gcc	aaa	336		
Ala	Gly	Leu	Arg	Asp	Ala	Ile	Ala	Glu	Lys	Gly	Gly	Asp	Pro	Ala	Lys			
			100				105						110					
gtg	aat	ccg	gtg	gtt	gca	aaa	ccc	agc	ttc	atc	gtc	gac	cac	tct	ctg	384		
Val	Asn	Pro	Val	Val	Ala	Lys	Pro	Ser	Phe	Ile	Val	Asp	His	Ser	Leu			
			115				120						125					
gcc	gtt	gaa	tgc	ggc	ggc	tac	gac	ccc	gat	gcc	ttc	cgc	aaa	aac	cgc	432		
Ala	Val	Glu	Cys	Gly	Gly	Tyr	Asp	Pro	Asp	Ala	Phe	Arg	Lys	Asn	Arg			
			130				135						140					
caa	atc	gaa	gac	aga	cgt	aac	gaa	gac	cgt	ttc	cac	ttc	atc	aac	tgg	480		
Gln	Ile	Glu	Asp	Arg	Arg	Asn	Glu	Asp	Arg	Phe	His	Phe	Ile	Asn	Trp			
			145				150						160					
aca	aaa	acc	gca	ttt	gaa	aat	gtg	gac	gtg	att	ccg	gcg	ggc	aac	ggc	528		
Thr	Lys	Thr	Ala	Phe	Glu	Asn	Val	Asp	Val	Ile	Pro	Ala	Gly	Asn	Gly			
			165						170						175			
atc	atg	cac	caa	atc	aat	cta	gaa	aaa	atg	tgc	ccc	gtc	gtc	caa	gtc	576		
Ile	Met	His	Gln	Ile	Asn	Leu	Glu	Lys	Met	Ser	Pro	Val	Val	Gln	Val			
			180						185						190			
aaa	aac	ggc	gtg	gcg	ttc	ccc	gat	acc	tgc	gtc	ggc	acg	gat	tgc	cac	624		
Lys	Asn	Gly	Val	Ala	Phe	Pro	Asp	Thr	Cys	Val	Gly	Thr	Asp	Ser	His			
			195			200						205						
acg	ccg	cac	gtc	gat	gcg	ctg	ggc	gtg	att	tcc	gtg	ggc	gtg	ggc	gga	672		
Thr	Pro	His	Val	Asp	Ala	Leu	Gly	Val	Ile	Ser	Val	Gly	Val	Gly	Gly			
			210			215						220						
ttg	gaa	gcg	gaa	acc	gtg	atg	ctg	ggt	cgc	gcg	tcc	atg	atg	cgc	ctg	720		
Leu	Glu	Ala	Glu	Thr	Val	Met	Leu	Gly	Arg	Ala	Ser	Met	Met	Arg	Leu			
			225			230						235			240			
ccc	gat	att	gtc	ggc	gtt	gag	ctg	aac	ggc	aaa	cgg	cag	gcg	ggc	att	768		
Pro	Asp	Ile	Val	Gly	Val	Glu	Leu	Asn	Gly	Lys	Arg	Gln	Ala	Gly	Ile			
			245						250						255			
acg	gcg	acg	gat	att	gtg	ttg	gca	ctg	acc	gag	ttt	ctg	cgc	aaa	gaa	816		
Thr	Ala	Thr	Asp	Ile	Val	Leu	Ala	Leu	Thr	Glu	Phe	Leu	Arg	Lys	Glu			
			260			265						270						
cgc	gtg	gtc	ggg	gcg	ttt	gtc	gaa	ttc	ttc	ggc	gag	ggc	gcg	aga	agc	864		
Arg	Val	Val	Gly	Ala	Phe	Val	Glu	Phe	Phe	Gly	Glu	Gly	Ala	Arg	Ser			
			275			280						285						
ctg	tct	atc	ggc	gac	cgc	gcg	acc	att	tcc	aac	atg	acg	ccg	gag	ttc	912		
Leu	Ser	Ile	Gly	Asp	Arg	Ala	Thr	Ile	Ser	Asn	Met	Thr	Pro	Glu	Phe			
			290			295						300						
ggc	gcg	act	gcc	gcg	atg	ttc	gct	att	gat	gag	caa	acc	att	gat	tat	960		

Leu	Lys	Leu	Thr	Gly	Arg	Asp	Asp	Ala	Gln	Val	Lys	Leu	Val	Glu	Thr	
				325					330					335		
tac	gcc	aaa	acc	gca	ggc	tta	tgg	gca	gat	gcc	ttg	aaa	acc	gcc	gtt	1056
Tyr	Ala	Lys	Thr	Ala	Gly	Leu	Trp	Ala	Asp	Ala	Leu	Lys	Thr	Ala	Val	
				340					345					350		
tat	ccg	cgc	gtt	ttg	aaa	ttt	gat	ttg	agc	agc	gta	acg	cgc	aat	atg	1104
Tyr	Pro	Arg	Val	Leu	Lys	Phe	Asp	Leu	Ser	Ser	Val	Thr	Arg	Asn	Met	
				355					360					365		
gca	ggc	ccg	agc	aac	ccg	cac	gcg	cgt	ttt	gcg	acc	gcc	gat	ttg	gcc	1152
Ala	Gly	Pro	Ser	Asn	Pro	His	Ala	Arg	Phe	Ala	Thr	Ala	Asp	Leu	Ala	
				370					375					380		
agc	aaa	ggc	ttg	gct	aaa	cct	tac	gaa	gag	cct	tca	gac	ggc	caa	atg	1200
Ser	Lys	Gly	Leu	Ala	Lys	Pro	Tyr	Glu	Glu	Pro	Ser	Asp	Gly	Gln	Met	
				385					390					395		
ccc	gac	ggc	gcg	gtc	atc	atc	gcc	gcg	att	acc	agt	tgc	acc	aac	act	1248
Pro	Asp	Gly	Ala	Val	Ile	Ile	Ala	Ala	Ile	Thr	Ser	Cys	Thr	Asn	Thr	
				405					410					415		
tcc	aac	ccg	cgc	aac	gtt	gtt	gcc	gcc	gcg	ctc	ttg	gcg	cgc	aac	gcc	1296
Ser	Asn	Pro	Arg	Asn	Val	Val	Ala	Ala	Ala	Leu	Leu	Ala	Arg	Asn	Ala	
				420					425					430		
aac	tgc	ttc	ggg	ctg	aaa	cgc	aaa	scg	tgg	gtc	aaa	acc	tgc	ttt	gcc	1344
Asn	Cys	Phe	Gly	Leu	Lys	Arg	Lys	Pro	Trp	Val	Lys	Thr	Ser	Phe	Ala	
				435					440					445		
ccc	ggt	tgc	aaa	gtg	gcg	gaa	att	tat	ttg	aaa	gaa	gca	ggc	ctg	ctg	1392
Pro	Gly	Ser	Lys	Val	Ala	Glu	Ile	Tyr	Leu	Lys	Glu	Ala	Gly	Leu	Leu	
				450					455					460		
ccc	gaa	atg	gaa	aaa	ctc	ggc	ttc	ggt	atc	gtc	gcc	ttc	gcc	tgc	acc	1440
Pro	Glu	Met	Glu	Lys	Leu	Gly	Phe	Gly	Ile	Val	Ala	Phe	Ala	Cys	Thr	
				465					470					475		
acc	tgc	aac	ggc	atg	agt	ggc	gcg	ctg	gat	ccg	aaa	atc	cag	aaa	gaa	1488
Thr	Cys	Asn	Gly	Met	Ser	Gly	Ala	Leu	Asp	Pro	Lys	Ile	Gln	Lys	Glu	
				485					490					495		
atc	atc	gac	cgc	gat	ttg	tac	gcc	acc	gcc	gta	tta	tca	ggc	aac	cgc	1536
Ile	Ile	Asp	Arg	Asp	Leu	Tyr	Ala	Thr	Ala	Val	Leu	Ser	Gly	Asn	Arg	
				500					505					510		
aac	ttc	gac	ggc	cgt	gtc	cat	ccg	tat	gcg	aaa	cag	gct	ttc	ctc	gct	1584
Asn	Phe	Asp	Gly	Arg	Val	His	Pro	Tyr	Ala	Lys	Gln	Ala	Phe	Leu	Ala	
				515					520					525		
tgc	cct	ccg	ttg	gtc	gtt	gcc	tac	gcg	ctg	gca	ggc	agt	atc	cgt	ttc	1632
Ser	Pro	Pro	Leu	Val	Val	Ala	Tyr	Ala	Leu	Ala	Gly	Ser	Ile	Arg	Phe	
				530					535					540		
gat	att	gaa	aac	gac	gta	ctc	ggc	gtt	gca	gac	ggc	aag	gaa	atc	cgc	1680
Asp	Ile	Glu	Asn	Asp	Val	Leu	Gly	Val	Ala	Asp	Gly	Lys</				

Leu	Lys	Asp	Ile	Trp	Pro	Ala	Asp	Glu	Glu	Ile	Asp	Ala	Val	Val	Ala				
																565	570	575	
gaa	tat	gtg	aaa	ccg	cag	cag	ttc	cgc	gat	gtg	tat	gta	ccg	atg	ttc	1776			
Glu	Tyr	Val	Lys	Pro	Gln	Gln	Phe	Arg	Asp	Val	Tyr	Val	Pro	Met	Phe				
																580	585	590	
gac	acc	ggc	aca	gcg	caa	aaa	gca	cct	agt	ccg	ctg	tac	gat	tgg	cgt	1824			
Asp	Thr	Gly	Thr	Ala	Gln	Lys	Ala	Pro	Ser	Pro	Leu	Tyr	Asp	Trp	Arg				
																595	600	605	
ccg	atg	tcc	acc	tac	atc	cgc	cgt	ccg	cct	tac	tgg	gaa	ggc	gcg	ctg	1872			
Pro	Met	Ser	Thr	Tyr	Ile	Arg	Arg	Pro	Pro	Tyr	Trp	Glu	Gly	Ala	Leu				
																610	615	620	
gca	ggg	gaa	cgc	aca	tta	aga	ggc	atg	cgt	ccg	ctg	gcg	att	ttg	ccc	1920			
Ala	Gly	Glu	Arg	Thr	Leu	Arg	Gly	Met	Arg	Pro	Leu	Ala	Ile	Leu	Pro				
																625	630	635	640
gac	aac	atc	acc	acc	gac	cac	ctc	tgc	ccg	tcc	aac	gcg	att	ttg	gcc	1968			
Asp	Asn	Ile	Thr	Thr	Asp	His	Leu	Ser	Pro	Ser	Asn	Ala	Ile	Leu	Ala				
																645	650	655	
gtc	agt	gcc	gca	ggc	gag	tat	ttg	gcg	aaa	atg	ggc	ttg	cct	gaa	gaa	2016			
Val	Ser	Ala	Ala	Gly	Glu	Tyr	Leu	Ala	Lys	Met	Gly	Leu	Pro	Glu	Glu				
																660	665	670	
gac	ttc	aac	tct	tac	gca	acc	cac	cgc	ggc	gac	cac	ttg	acc	gcc	caa	2064			
Asp	Phe	Asn	Ser	Tyr	Ala	Thr	His	Arg	Gly	Asp	His	Leu	Thr	Ala	Gln				
																675	680	685	
cgc	gct	acc	ttc	gcc	aac	ccg	aaa	ctg	ttt	aac	gaa	atg	gtg	aaa	aac	2112			
Arg	Ala	Thr	Phe	Ala	Asn	Pro	Lys	Leu	Phe	Asn	Glu	Met	Val	Lys	Asn				
																690	695	700	
gaa	gac	ggc	agc	gtg	cgc	caa	ggc	tgc	ttc	gcc	cgc	gtc	gaa	ccc	gaa	2160			
Glu	Asp	Gly	Ser	Val	Arg	Gln	Gly	Ser	Phe	Ala	Arg	Val	Glu	Pro	Glu				
																705	710	715	720
ggc	gaa	acc	atg	cgc	atg	tgg	gaa	gcc	atc	gaa	acc	tat	atg	aac	cgc	2208			
Gly	Glu	Thr	Met	Arg	Met	Trp	Glu	Ala	Ile	Glu	Thr	Tyr	Met	Asn	Arg				
																725	730	735	
aaa	cag	ccg	ctc	atc	atc	att	gcc	ggt	gcg	gac	tat	ggt	caa	ggc	tca	2256			
Lys	Gln	Pro	Leu	Ile	Ile	Ile	Ala	Gly	Ala	Asp	Tyr	Gly	Gln	Gly	Ser				
																740	745	750	
agc	cgc	gac	tgg	gct	gca	aaa	ggc	gta	cgc	ctc	gcc	ggc	gta	gaa	gcg	2304			
Ser	Arg	Asp	Trp	Ala	Ala	Lys	Gly	Val	Arg	Leu	Ala	Gly	Val	Glu	Ala				
																755	760	765	
att	gtt	gcc	gaa	ggc	ttc	gag	cgt	atc	cac	cgc	acc	aac	ctt	atc	ggc	2352			
Ile	Val	Ala	Glu	Gly	Phe	Glu	Arg	Ile	His	Arg	Thr	Asn	Leu	Ile	Gly				
																770	775	780	
atg	ggc	gtg	ttg	ccg	ctg	cag	ttc	aaa	ccc	gac	acc	aac	cgc	cat	acc	2400			
Met	Gly	Val	Leu	Pro	Leu	Gln	Phe	Lys	Pro	Asp	Thr	Asn	Arg	His	Thr				
																785	790	795	800
ctg	caa	ctg	gac	ggc	acg	gaa	acc	tac	gac	gtg	gtc	ggc	gaa	cgc	aca	2448			

Leu Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr  
805 810 815  
cgc cgc tgc gac ctg acc ctc gtg att cac cgt aaa aac ggc gaa acc 2496  
Pro Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr  
820 825 830  
gtc gaa gtt ccc gtt acc tgc cgc ctc gat act gca gaa gaa gta ttg 2544  
Val Glu Val Pro Val Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu  
835 840 845  
gta tat gaa gcc ggc ggc gtg ttg caa cgg ttt gca cag gat ttt ttg 2592  
Val Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu  
850 855 860  
gaa ggg aac gcg gct tag 2610  
Glu Gly Asn Ala Ala  
865

<210> 42  
<211> 869  
<212> PRT  
<213> Neisseria meningitidis

<400> 42  
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1 5 10 15  
Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Asp Ile Lys Pro Gly Ser  
20 25 30  
Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val  
35 40 45  
Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly  
50 55 60  
Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala  
65 70 75 80  
Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu  
85 90 95  
Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys  
100 105 110  
Val Asn Pro Val Val Ala Lys Pro Ser Phe Ile Val Asp His Ser Leu  
115 120 125  
Ala Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg  
130 135 140  
Gln Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp  
145 150 155 160  
Thr Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly  
165 170 175  
Ile Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val

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180	185	190
Lys Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His 195	200	205
Thr Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly 210	215	220
Leu Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu 225	230	235 240
Pro Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Gln Ala Gly Ile 245	250	255
Thr Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu 260	265	270
Arg Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser 275	280	285
Leu Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe 290	295	300
Gly Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr 305	310	315 320
Leu Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr 325	330	335
Tyr Ala Lys Thr Ala Gly Leu Trp Ala Asp Ala Leu Lys Thr Ala Val 340	345	350
Tyr Pro Arg Val Leu Lys Phe Asp Leu Ser Ser Val Thr Arg Asn Met 355	360	365
Ala Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala 370	375	380
Ser Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met 385	390	395 400
Pro Asp Gly Ala Val Ile Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr 405	410	415
Ser Asn Pro Arg Asn Val Val Ala Ala Ala Leu Leu Ala Arg Asn Ala 420	425	430
Asn Cys Phe Gly Leu Lys Arg Lys Pro Trp Val Lys Thr Ser Phe Ala 435	440	445
Pro Gly Ser Lys Val Ala Glu Ile Tyr Leu Lys Glu Ala Gly Leu Leu 450	455	460
Pro Glu Met Glu Lys Leu Gly Phe Gly Ile Val Ala Phe Ala Cys Thr 465	470	475 480
Thr Cys Asn Gly Met Ser Gly Ala Leu Asp Pro Lys Ile Gln Lys Glu 485	490	495
Ile Ile Asp Arg Asp Leu Tyr Ala Thr Ala Val Leu Ser Gly Asn Arg		

0930433 061601

500	505	510
Asn Phe Asp Gly Arg Val His	Pro Tyr Ala Lys Gln Ala Phe Leu Ala	
515	520	525
Ser Pro Pro Leu Val Val Ala Tyr Ala Leu Ala Gly Ser Ile Arg Phe		
530	535	540
Asp Ile Glu Asn Asp Val Leu Gly Val Ala Asp Gly Lys Glu Ile Arg		
545	550	555
Leu Lys Asp Ile Trp Pro Ala Asp Glu Glu Ile Asp Ala Val Val Ala		
	565	570
Glu Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Val Pro Met Phe		
	580	585
Asp Thr Gly Thr Ala Gln Lys Ala Pro Ser Pro Leu Tyr Asp Trp Arg		
	595	600
Pro Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu		
	610	615
Ala Gly Glu Arg Thr Leu Arg Gly Met Arg Pro Leu Ala Ile Leu Pro		
	625	630
Asp Asn Ile Thr Thr Asp His Leu Ser Pro Ser Asn Ala Ile Leu Ala		
	645	650
Val Ser Ala Ala Gly Glu Tyr Leu Ala Lys Met Gly Leu Pro Glu Glu		
	660	665
Asp Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln		
	675	680
Arg Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Lys Asn		
	690	695
Glu Asp Gly Ser Val Arg Gln Gly Ser Phe Ala Arg Val Glu Pro Glu		
	705	710
Gly Glu Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg		
	725	730
Lys Gln Pro Leu Ile Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser		
	740	745
Ser Arg Asp Trp Ala Ala Lys Gly Val Arg Leu Ala Gly Val Glu Ala		
	755	760
Ile Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly		
	770	775
Met Gly Val Leu Pro Leu Gln Phe Lys Pro Asp Thr Asn Arg His Thr		
	785	790
Leu Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr		
	805	810
Pro Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr		

0930433-084604

830

Glu Gly Asn Ala Ala  
865

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<210> 43
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<212> DNA
<213> Neisseria meningitidis
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<220>
<221> CDS
<222> (1) .. (1167)
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145 150 155 160	
ctc gac ggc gta acg ttc ccg gca gcc gaa gta caa atc gaa ttt ctt	528
Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu	
165 170 175	
gat cca gcc gac ggc gaa ggc agt atg ttc cca acc ggc aat ttg gtc	576
Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val	
180 185 190	
gat gaa att gat gtg ccg aat ata ggc cgt ttg aaa gcc acg ctc atc	624
Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile	
195 200 205	
aac gcg ggc att ccg acc gtt ttc ctg aat gcc gcc gac ttg ggc tac	672
Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr	
210 215 220	
acg ggc aaa gag ttg caa gac gac atc aac aac gat gcc gca gct ttg	720
Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu	
225 230 235 240	
gaa aaa ttc gag aaa atc cgc gct tac ggt gcg ctg aaa atg ggt cta	768
Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu	
245 250 255	
atc agc gac gta tcc gaa gct gcc gcc cgc gcg cac acg ccg aaa gtc	816
Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val	
260 265 270	
gcc ttc gtc gcg ccc gcc gcc gat tac acc gcc tcc agt ggc aaa acc	864
Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr	
275 280 285	
gtg aat gcc gcc gac atc gat ttg ctg gta cgc gcc ctg agc atg gcc	912
Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly	
290 295 300	
aaa ttg cac cac gcg atg atg ggt acc gcc tct gtt gcc att gcg acc	960
Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr	
305 310 315 320	
gcc gcc gcc gtg ccc ggt acg ctg gtc aac ctt gcc gca ggg gcg gga	1008
Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Ala Gly	
325 330 335	
acg cgt aaa gaa gtg cgc ttc ggg cat cct tcc ggc aca ttg cgc gtc	1056
Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val	
340 345 350	
ggt gca gcc gcc gaa tgt cag gac gga caa tgg acg gcc acc aaa gcg	1104
Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala	
355 360 365	
gtt atg agc cgc agc gca cgc gtg atg atg gaa ggt tgg gtc agg gtg	1152
Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val	
370 375 380	
ccg gaa gat tgt ttt taa	1170
Pro Glu Asp Cys Phe	
385	

<210> 44  
 <211> 389  
 <212> PRT

09830433-081604

<213> Neisseria meningitidis

<400> 44

Met	Pro	Gln	Ile	Lys	Ile	Pro	Ala	Val	Tyr	Tyr	Arg	Gly	Gly	Thr	Ser	1	5	10	15
Lys	Gly	Val	Phe	Phe	Lys	Arg	Ser	Asp	Leu	Pro	Glu	Ala	Ala	Arg	Glu	20	25	30	
Ala	Gly	Ser	Ala	Arg	Asp	Lys	Ile	Leu	Leu	Arg	Val	Leu	Gly	Ser	Pro	35	40	45	
Asp	Pro	Tyr	Gly	Lys	Gln	Ile	Asp	Gly	Leu	Gly	Asn	Ala	Ser	Ser	Ser	50	55	60	
Thr	Ser	Lys	Ala	Val	Ile	Leu	Asp	Lys	Ser	Glu	Arg	Thr	Asp	His	Asp	65	70	75	80
Val	Asp	Tyr	Leu	Phe	Gly	Gln	Val	Ser	Ile	Asp	Lys	Pro	Phe	Val	Asp	85	90	95	
Trp	Ser	Gly	Asn	Cys	Gly	Asn	Leu	Thr	Ala	Ala	Val	Gly	Ala	Phe	Ala	100	105	110	
Ile	Glu	Gln	Gly	Leu	Val	Asp	Lys	Ser	Lys	Ile	Pro	Ser	Asp	Gly	Pro	115	120	125	
Cys	Thr	Val	Lys	Ile	Trp	Gln	Lys	Asn	Ile	Gly	Lys	Thr	Ile	Ile	Ala	130	135	140	
His	Val	Pro	Met	Gln	Asn	Gly	Ala	Val	Leu	Glu	Thr	Gly	Asp	Phe	Glu	145	150	155	160
Leu	Asp	Gly	Val	Thr	Phe	Pro	Ala	Ala	Glu	Val	Gln	Ile	Glu	Phe	Leu	165	170	175	
Asp	Pro	Ala	Asp	Gly	Glu	Gly	Ser	Met	Phe	Pro	Thr	Gly	Asn	Leu	Val	180	185	190	
Asp	Glu	Ile	Asp	Val	Pro	Asn	Ile	Gly	Arg	Leu	Lys	Ala	Thr	Leu	Ile	195	200	205	
Asn	Ala	Gly	Ile	Pro	Thr	Val	Phe	Leu	Asn	Ala	Ala	Asp	Leu	Gly	Tyr	210	215	220	
Thr	Gly	Lys	Glu	Leu	Gln	Asp	Asp	Ile	Asn	Asn	Asp	Ala	Ala	Ala	Leu	225	230	235	240
Glu	Lys	Phe	Glu	Lys	Ile	Arg	Ala	Tyr	Gly	Ala	Leu	Lys	Met	Gly	Leu	245	250	255	
Ile	Ser	Asp	Val	Ser	Glu	Ala	Ala	Ala	Arg	Ala	His	Thr	Pro	Lys	Val	260	265	270	

05B30433-08160

Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr  
 275 280 285

Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly  
 290 295 300

Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr  
 305 310 315 320

Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Ala Gly  
 325 330 335

Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val  
 340 345 350

Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala  
 355 360 365

Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val  
 370 375 380

Pro Glu Asp Cys Phe  
 385

<210> 45  
 <211> 954  
 <212> DNA  
 <213> Neisseria meningitidis

<220>  
 <221> CDS  
 <222> (1) .. (951)

<400> 45  
 atg cgc acg ccc ttt tgt tgg gca tac gcc aat gcc gcc cga ata tcg 48  
 Met Arg Thr Pro Phe Cys Trp Ala Tyr Ala Asn Ala Ala Arg Ile Ser  
 1 5 10 15

gca atg ctg ccc gcc tgt tgg gcc cag gcc atg ttg gcc gaa gta atc 96  
 Ala Met Leu Pro Ala Cys Trp Ala Gln Ala Met Leu Ala Glu Val Ile  
 20 25 30

agc tgc aac aag gct tgg tgg ctg ccg cag cct tgg gcc aga tgg gcc 144  
 Ser Cys Asn Lys Ala Ser Ser Leu Pro Gln Pro Ser Ala Arg Ser Ala  
 35 40 45

ttt aaa tca acc tgc ttc atg ggt gat tct ccg tat ttg gtt cag ata 192  
 Phe Lys Ser Thr Cys Phe Met Gly Asp Ser Pro Tyr Leu Val Gln Ile  
 50 55 60

gac ttg gtt ttt gcc ccc cag gcc ggt gcc ttc ttt caa gcc gat tat 240  
 Asp Leu Val Phe Ala Pro Gln Gly Gly Gly Phe Phe Gln Ala Asp Tyr  
 65 70 75 80

ttt gaa ttt gac ttt gct gcc gaa gcc cag ctg tgc cag cct gcc caa 288  
 Phe Glu Phe Asp Phe Ala Ala Glu Ala His Leu Cys Gln Pro Ala Gln  
 85 90 95

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<210> 46
<211> 317
<212> PRT
<213> Neisseria meningitidis
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<400> 46

Met Arg Thr Pro Phe Cys Trp Ala Tyr Ala Asn Ala Ala Arg Ile Ser  
 1 5 10 15

Ala Met Leu Pro Ala Cys Trp Ala Gln Ala Met Leu Ala Glu Val Ile  
 20 25 30

Ser Cys Asn Lys Ala Ser Ser Leu Pro Gln Pro Ser Ala Arg Ser Ala  
 35 40 45

Phe Lys Ser Thr Cys Phe Met Gly Asp Ser Pro Tyr Leu Val Gln Ile  
 50 55 60

Asp Leu Val Phe Ala Pro Gln Gly Gly Gly Phe Phe Gln Ala Asp Tyr  
 65 70 75 80

Phe Glu Phe Asp Phe Ala Ala Glu Ala His Leu Cys Gln Pro Ala Gln  
 85 90 95

Ile Gly Gly Gly Asn Gly Ser Asp Phe Arg Ile Thr Ala Gly Gly Leu  
 100 105 110

Arg Ile Gly Gln Gln Asp Asn Arg Phe Ala Ala Gly Arg His Leu His  
 115 120 125

Gly Ser Cys Leu Asn Ser Val Gly Gln His Phe Gln Arg Leu Arg Gln  
 130 135 140

Gly Gln Arg Leu Ser Val Glu Ala Val Ala His Ala Val Ala Ile Ala  
 145 150 155 160

Leu Gln Arg Pro Arg Phe Pro Phe Gln Ile Gln Thr Pro Phe Phe Thr  
 165 170 175

Glu Ser Gly Ile Phe Arg Arg Arg Asn Lys Val Asp Gly Ile Gly Lys  
 180 185 190

Arg Tyr Arg Gly Asn Ala Asp Phe Gly Gln Phe Leu Arg Thr Phe Ala  
 195 200 205

Asp Gly Glu Ile Ile Ala Phe Leu Gln His Ser Ala Leu Met Ala Ala  
 210 215 220

Glu Thr Gly Phe Gln Val Gly Ala Ser Arg Thr His His Phe Arg His  
 225 230 235 240

Ile Lys Ser Ala Arg His Ala His Ile Ala Val His Ala Leu His Gly  
 245 250 255

Thr His His Phe Gln Gly Leu Pro Phe Ala Gly Gly Ile Thr Pro Ile  
 260 265 270

Arg Ile Asp Arg Phe Ala Val Gln Phe Arg Leu Ile His Gly Thr Gly  
 275 280 285

Glu Thr Lys Arg Arg Ile Pro Phe Lys His Gln His Tyr Pro Ala Gln  
 290 295 300

Ser Asp Phe Asp Cys Gly Arg Ala Phe Val Val Ala Gln  
 305 310 315

<210> 47

FOOTNOTES

<211> 648  
 <212> DNA  
 <213> Neisseria meningitidis

<220>  
 <221> CDS  
 <222> (1)..(645)

<400> 47  
 atg aga ata gag atc aca cca atc agc gaa tcc gct ttg gtc tgc cga 48  
 Met Arg Ile Glu Ile Thr Pro Ile Ser Glu Ser Ala Leu Val Cys Arg  
 1 5 10 15

ctg aat gcg cct tcc gaa ctg ggc aaa cag caa aag ttg tgg gcg ttc 96  
 Leu Asn Ala Pro Ser Glu Leu Gly Lys Gln Gln Lys Leu Trp Ala Phe  
 20 25 30

gcc gct gcg ctc ggg cag cac gac agg att gag gaa gtg gtg gtc ggc 144  
 Ala Ala Ala Leu Gly Gln His Asp Arg Ile Glu Glu Val Val Val Gly  
 35 40 45

atg aac aat ctg acc gtc ttc acc cgt ttc gat acc gat ttg gcg acg 192  
 Met Asn Asn Leu Thr Val Phe Thr Arg Phe Asp Thr Asp Leu Ala Thr  
 50 55 60

ctt gcc gat gaa ttg caa tat gtg tgg gaa cac acc gcc gct aca gac 240  
 Leu Ala Asp Glu Leu Gln Tyr Val Trp Glu His Thr Ala Val Thr Asp  
 65 70 75 80

cat cag ggc aaa ctg gtg gaa att ccc gtc tgc tac ggc ggc gaa tac 288  
 His Gln Gly Lys Leu Val Glu Ile Pro Val Cys Tyr Gly Gly Glu Tyr  
 85 90 95

ggc ccg gat ttg gcg gaa gtc gct gct ttc cat cag acg gcc att tcc 336  
 Gly Pro Asp Leu Ala Glu Val Ala Ala Phe His Gln Thr Val Ile Ser  
 100 105 110

gaa atc gtc cgc cgc cat acg gcg caa att tat acc gta ttt atg atg 384  
 Glu Ile Val Arg Arg His Thr Ala Gln Thr Tyr Thr Val Phe Met Met  
 115 120 125

ggc ttc cag cct ggt ttc cct tat ctg ggc ggc ttg ccc gaa gca ttg 432  
 Gly Phe Gln Pro Gly Phe Pro Tyr Leu Gly Gly Leu Pro Glu Ala Leu  
 130 135 140

cac acg ccc cgc cgt gcc gtc ccg aga acg tcc gtt cct gcc ggt tgc 480  
 His Thr Pro Arg Arg Ala Val Pro Arg Thr Ser Val Pro Ala Gly Ser  
 145 150 155 160

gtc ggt atc gcc gcc agt cag acc ggt gtg tat ccg ttc gct tgc ccc 528  
 Val Gly Ile Gly Gly Ser Gln Thr Gly Val Tyr Pro Phe Ala Ser Pro  
 165 170 175

109780-CC40E360

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ggc ggc tgg cag att atc ggc aga acc gaa tta ccc ttg ttc cga gcc 576
Gly Gly Trp Gln Ile Ile Gly Arg Thr Glu Leu Pro Leu Phe Arg Ala
      180                      185                      190

gat ttg aat ccg ccg acc ctg ctg gcg gcg ggt gac caa gtc cgc ttt 624
Asp Leu Asn Pro Pro Thr Leu Leu Ala Ala Gly Asp Gln Val Arg Phe
      195                      200                      205

gtt gca gaa agg att gag cca tga 648
Val Ala Glu Arg Ile Glu Pro
      210                      215

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<210> 48  
 <211> 215  
 <212> PRT  
 <213> Neisseria meningitidis

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<400> 48
Met Arg Ile Glu Ile Thr Pro Ile Ser Glu Ser Ala Leu Val Cys Arg
  1                      5                      10                      15

Leu Asn Ala Pro Ser Glu Leu Gly Lys Gln Gln Lys Leu Trp Ala Phe
      20                      25                      30

Ala Ala Ala Leu Gly Gln His Asp Arg Ile Glu Glu Val Val Val Gly
      35                      40                      45

Met Asn Asn Leu Thr Val Phe Thr Arg Phe Asp Thr Asp Leu Ala Thr
      50                      55                      60

Leu Ala Asp Glu Leu Gln Tyr Val Trp Glu His Thr Ala Val Thr Asp
      65                      70                      75                      80

His Gln Gly Lys Leu Val Glu Ile Pro Val Cys Tyr Gly Gly Glu Tyr
      85                      90                      95

Gly Pro Asp Leu Ala Glu Val Ala Ala Phe His Gln Thr Val Ile Ser
      100                      105                      110

Glu Ile Val Arg Arg His Thr Ala Gln Thr Tyr Thr Val Phe Met Met
      115                      120                      125

Gly Phe Gln Pro Gly Phe Pro Tyr Leu Gly Gly Leu Pro Glu Ala Leu
      130                      135                      140

His Thr Pro Arg Arg Ala Val Pro Arg Thr Ser Val Pro Ala Gly Ser
      145                      150                      155                      160

Val Gly Ile Gly Gly Ser Gln Thr Gly Val Tyr Pro Phe Ala Ser Pro
      165                      170                      175

Gly Gly Trp Gln Ile Ile Gly Arg Thr Glu Leu Pro Leu Phe Arg Ala
      180                      185                      190

Asp Leu Asn Pro Pro Thr Leu Leu Ala Ala Gly Asp Gln Val Arg Phe
      195                      200                      205

Val Ala Glu Arg Ile Glu Pro
      210                      215

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09630433-081604

<210> 49  
 <211> 930  
 <212> DNA  
 <213> Neisseria meningitidis

<220>  
 <221> CDS  
 <222> (1)..(927)

<400> 49  
 atg att cac gtt tgc gca gtg cag gca ccg gcg cat att cag gat acc 48  
 Met Ile His Val Ser Ala Val Gln Ala Pro Ala His Ile Gln Asp Thr  
 1 5 10 15  
 gga cgc tac gga cac cgg cgt tac ggc atc ggt cat gcc ggt gcg atg 96  
 Gly Arg Tyr Gly His Arg Arg Tyr Gly Ile Gly His Ala Gly Ala Met  
 20 25 30  
 gac acg gtt gct ttg gcg gcg ggt aat att tta tgc ggc aac gac gaa 144  
 Asp Thr Val Ala Leu Ala Ala Gly Asn Ile Leu Leu Gly Asn Asp Glu  
 35 40 45  
 ggc acg gcc gca atc gaa atc gct ttg ggc ggg ata atg ctg gtg ttt 192  
 Gly Thr Ala Ala Ile Glu Ile Ala Leu Gly Gly Ile Met Leu Val Phe  
 50 55 60  
 gaa cgg gat acg ccg ttt tgt ctc acc gat gcc gcg tat cag gcc gaa 240  
 Glu Arg Asp Thr Pro Phe Cys Leu Thr Gly Ala Val Tyr Gln Ala Glu  
 65 70 75 80  
 ttg gac gcc gaa ccg gtc tat tgc tat tgg cgt tat acc gcc cgc aaa 288  
 Leu Asp Gly Glu Pro Val Tyr Ser Tyr Trp Arg Tyr Thr Ala Arg Lys  
 85 90 95  
 ggg cag acc ttg aaa atg gtg cgt gcc gtg cag gcc atg tac gcc tat 336  
 Gly Gln Thr Leu Lys Met Val Arg Ala Val Gln Gly Met Tyr Gly Tyr  
 100 105 110  
 gtg tgc gtg gcg gcc gga ttt gat gtg ccg gaa gtg atg ggt tgc aga 384  
 Val Cys Val Ala Gly Gly Phe Asp Val Pro Glu Val Met Gly Ser Arg  
 115 120 125  
 agc acc gac ctg aaa gcc ggt ttc ggc gcc cat cag gcc aga atg ctg 432  
 Ser Thr Asp Leu Lys Ala Gly Phe Gly Gly His Gln Gly Arg Met Leu  
 130 135 140  
 caa aaa gcc gat tat ctc ccc atc gcc aaa ggt gcg cag gaa ttg tcc 480  
 Gln Lys Gly Asp Tyr Leu Pro Ile Gly Lys Gly Ala Gln Glu Leu Ser  
 145 150 155 160  
 aaa gtc gcc att gcc ccg ata ccg ttt acc gat acc atc cac ctt gtt 528  
 Lys Val Gly Ile Ala Pro Ile Pro Phe Thr Asp Thr Ile His Leu Val  
 165 170 175  
 cct tgc tgc gaa tat gcc gct ttc agt gaa aaa ggg cgt ctg aat ctg 576  
 Pro Ser Ser Glu Tyr Ala Ala Phe Ser Glu Lys Gly Arg Leu Asn Leu  
 180 185 190

09830433 081601

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<210> 50
<211> 309
<212> PRT
<213> Neisseria meningitidis
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Met	Ile	His	Val	Ser	Ala	Val	Gln	Ala	Pro	Ala	His	Ile	Gln	Asp	Thr
1				5					10					15	
Gly	Arg	Tyr	Gly	His	Arg	Arg	Tyr	Gly	Ile	Gly	His	Ala	Gly	Ala	Met
			20					25					30		
Asp	Thr	Val	Ala	Leu	Ala	Ala	Gly	Asn	Ile	Leu	Leu	Gly	Asn	Asp	Glu
		35					40					45			
Gly	Thr	Ala	Ala	Ile	Gln	Ile	Ala	Leu	Gly	Gly	Ile	Met	Leu	Val	Phe
		50				55					60				
Glu	Arg	Asp	Thr	Pro	Phe	Cys	Leu	Thr	Gly	Ala	Val	Tyr	Gln	Ala	Glu
65					70					75					80
Leu	Asp	Gly	Glu	Pro	Val	Tyr	Ser	Tyr	Trp	Arg	Tyr	Thr	Ala	Arg	Lys
				85					90					95	
Gly	Gln	Thr	Leu	Lys	Met	Val	Arg	Ala	Val	Gln	Gly	Met	Tyr	Gly	Tyr
			100					105					110		

Val Cys Val Ala Gly Gly Phe Asp Val Pro Glu Val Met Gly Ser Arg  
 115 120 125

Ser Thr Asp Leu Lys Ala Gly Phe Gly Gly His Gln Gly Arg Met Leu  
 130 135 140

Gln Lys Gly Asp Tyr Leu Pro Ile Gly Lys Gly Ala Gln Glu Leu Ser  
 145 150 155 160

Lys Val Gly Ile Ala Pro Ile Pro Phe Thr Asp Thr Ile His Leu Val  
 165 170 175

Pro Ser Ser Glu Tyr Ala Ala Phe Ser Glu Lys Gly Arg Leu Asn Leu  
 180 185 190

Glu Arg Glu Thr Trp Thr Leu Gln Ser Asp Ser Asn Arg Met Gly Tyr  
 195 200 205

Arg Phe Asp Gly Gln Pro Leu Thr Leu Ser Gln Pro Leu Glu Met Leu  
 210 215 220

Ser His Ala Val Gln Ala Gly Thr Val Gln Val Pro Pro Gly Gly Lys  
 225 230 235 240

Pro Ile Ile Leu Leu Ala Asp Ala Gln Thr Thr Gly Gly Tyr Pro Lys  
 245 250 255

Ile Ala Thr Val Ala Ala Ala Asp Leu Gly Arg Leu Ala Gln Val Arg  
 260 265 270

Phe Gly Ser Lys Val Lys Phe Lys Ile Ile Gly Leu Lys Glu Ala Thr  
 275 280 285

Ala Leu Arg Arg Lys Asn Gln Val Tyr Leu Asn Gln Ile Arg Arg Ile  
 290 295 300

Thr His Glu Ala Gly  
 305

<210> 51  
 <211> 2094  
 <212> DNA  
 <213> Neisseria meningitidis

<220>  
 <221> CDS  
 <222> (1)..(2091)

<400> 51  
 atg aat tgg acc gaa agt aaa acc ctg aaa gga tgg tgg ctg gtg ttt 48  
 Met Asn Ser Thr Ala Ser Lys Thr Leu Lys Gly Leu Ser Leu Val Phe  
 1 5 10 15

tgc gcc tct gga ttc tgc gcc ctg att tac cag gtc agc tgg cag agg 96  
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Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile	
35 40 45	
att tct gta ttt atg gtc ggc ttg ggt gta ggt gcg tat ttc ggt gga	192
Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly	
50 55 60	
cgc att gct gac cgt ttt cct tca agt atc atc ccc ctg ttt tgc atc	240
Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile	
65 70 75 80	
gct gaa gta tcc atc ggt ctg ttc ggt ttg gta agc agg ggt ctg att	288
Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Arg Gly Leu Ile	
85 90 95	
tcc gcc ttg ggg cag ctc tta gtt gag gct gat ttg ccc atc atc gct	336
Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala	
100 105 110	
gct gcc aat ttc ctc tta ttg ctg ctc cct acc ttt atg atg ggc gcg	384
Ala Ala Asn Phe Leu Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala	
115 120 125	
acc ttg ccc ttg ctg acc tgt ttt ttt aac cgg aaa ata cat aat gct	432
Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val	
130 135 140	
ggc gag tct atc ggt acc tta tat ttt ttc aac act ttg ggt gcg gca	480
Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala	
145 150 155 160	
ccc gga tcc ctc gcc gcc gcc gaa ttt tta taa gtc tta ttt acc ctc	528
Leu Gly Ser Leu Ala Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu	
165 170 175	
tcc caa acc att gcc ctg aca gcc cgc ttt aac ctt ctg att gct gct	576
Ser Gln Thr Ile Ala Leu Thr Ala Cys Phe Asn Leu Leu Ile Ala Ala	
180 185 190	
tca gta tgc tgc gtt aca gaa agg atg gat ata gtc aac act aaa cgg	624
Ser Val Cys Cys Val Thr Glu Arg Met Asp Ile Val Asn Thr Lys Pro	
195 200 205	
aat act agt ttg att tat atg ctt tct ttc ctt agc ggt tta ttg agc	672
Asn Thr Ser Leu Ile Tyr Met Leu Ser Phe Leu Ser Gly Leu Leu Ser	
210 215 220	
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Leu Gly Ile Glu Val Leu Trp Val Arg Met Phe Ser Phe Ala Ala Gln	
225 230 235 240	
tcc gtg cct cag gca ttt tca att act ctt gcc tat ttt ctg acc ggt	768
Ser Val Pro Gln Ala Phe Ser Phe Thr Leu Ala Tyr Phe Leu Thr Gly	
245 250 255	
atc gcc gtc ggc gcc tat ttt gcc aaa cgg att tgc cgc agc cgc ttt	816
Ile Ala Val Gly Ala Tyr Phe Gly Lys Arg Ile Cys Arg Ser Arg Phe	
260 265 270	

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gtt gat att ccc ttt atc ggg cag tgc ttc ttg ttg ggc ggt att gcc	864
Val Asp Ile Pro Phe Ile Gly Gln Cys Phe Leu Trp Ala Gly Ile Ala	
275	280
gac ttt ttg att ttg ggt gct gcg tgg ttg ttg acg ggt ttt tcc ggc	912
Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly	
290	295
300	
ttc gtc cac cac gcc ggt atc ttc att acc ctg tct gcc gtc gtc aga	960
Phe Val His His Ala Gly Ile Phe Ile Thr Leu Ser Ala Val Val Arg	
305	310
315	320
ggg ttg att ttc ccg ctg gta cac cat gtg ggt acg gat ggc aac aaa	1008
Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys	
325	330
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tcc gga cga cag gtt tcc aat gtt tat ttc gcc aac gtt gcc ggc agt	1056
Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser	
340	345
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gca ttg ggt ccg gtc ctt atc ggc ttt gtg ata ctt gat ttc ttg tcc	1104
Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Phe Leu Ser	
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acc caa cag att tac ctg ttc atc tgt ttg att tct gct gct gtc cct	1152
Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro	
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ttg ttc tgt aca ctg ttc caa aaa agt ctg cga ctg aat gca gtg tgg	1200
Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser	
385	390
395	400
gta gca ggt tcc cta atg ttc ggc atc ctg atg ttc cta ctg ccg gat	1248
Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp	
405	410
415	
tct gtc ttc caa aat att gct gac cgt ccg gat cgg ctg att gaa aac	1296
Ser Val Phe Gln Asn Ile Ala Asp Arg Pro Asp Arg Leu Ile Glu Asn	
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430	
aaa cac ggc att gct gcg gtt tac cat aga gat ggt gat aag gtt gtt	1344
Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val	
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445	
tat ggg gcg aat gta tac gac ggc gca tac aat acc gat gta ttc aat	1392
Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Val Phe Asn	
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460	
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Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser	
465	470
475	480
ggc ata cgc cgc att ttc gtc gtt gga ttg agt aca ggt tgg tgg gcg	1488
Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala	
485	490
495	
cgc gtc ttg tct gcc att ccg gaa atg cag tgg atg atc gtt ggc gaa	1536
Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu	
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510	

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Ile	Asn	Pro	Ala	Tyr	Arg	Ser	Leu	Ile	Ala	Asp	Glu	Pro	Gln	Ile	Ala	
		515					520					525				
ccg	ctt	ttg	cag	gac	aaa	cgt	gtt	gaa	att	gta	ttg	gat	gac	ggc	agg	1632
Pro	Leu	Leu	Gln	Asp	Lys	Arg	Val	Glu	Ile	Val	Leu	Asp	Asp	Gly	Arg	
		530				535					540					
aaa	tgg	ctg	cgt	cgc	cat	ccg	gat	gaa	aaa	ttc	gac	ctg	att	ttg	atg	1680
Lys	Trp	Leu	Arg	Arg	His	Pro	Asp	Glu	Lys	Phe	Asp	Leu	Ile	Leu	Met	
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Asn	Thr	Thr	Trp	Tyr	Trp	Arg	Ala	Tyr	Ser	Thr	Asn	Leu	Leu	Ser	Ala	
				565					570					575		
gaa	ttt	tta	aaa	cag	gtg	caa	agc	cac	ctt	acc	ccg	gat	ggc	att	gta	1776
Glu	Phe	Leu	Lys	Gln	Val	Gln	Ser	His	Leu	Thr	Pro	Asp	Gly	Ile	Val	
			580					585					590			
atg	ttt	aat	acc	acg	cac	agc	ccg	cat	gct	ttt	gct	acc	gcc	gta	cac	1824
Met	Phe	Asn	Thr	Thr	His	Ser	Pro	His	Ala	Phe	Ala	Thr	Ala	Val	His	
		595					600					605				
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Ser	Ile	Pro	Tyr	Ala	Tyr	Arg	Tyr	Gly	His	Met	Val	Val	Gly	Ser	Ala	
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acc	ccg	gta	gct	ttc	ccc	aat	aaa	gaa	ctg	ctc	aag	caa	cgt	ctc	tcg	1920
Thr	Pro	Val	Val	Phe	Pro	Asn	Lys	Glu	Leu	Leu	Lys	Gln	Arg	Leu	Ser	
		625				630					635				640	
agg	ttg	att	tgg	ccg	gaa	agc	ggc	agg	cac	gta	ttt	gac	agc	agg	acc	1968
Arg	Leu	Ile	Trp	Pro	Glu	Ser	Gly	Arg	His	Val	Phe	Asp	Ser	Ser	Thr	
				645				650						655		
gtg	gat	gct	gca	gca	caa	aag	gct	gtc	tcg	cgt	atg	ctg	att	cag	atg	2016
Val	Asp	Ala	Ala	Ala	Gln	Lys	Val	Val	Ser	Arg	Met	Leu	Ile	Gln	Met	
			660					665						670		
acg	gaa	ccc	tcg	gct	ggg	gcg	gaa	gtc	att	acc	gac	gat	aat	atg	att	2064
Thr	Glu	Pro	Ser	Ala	Gly	Ala	Glu	Val	Ile	Thr	Asp	Asp	Asn	Met	Ile	
		675				680						685				
gta	gaa	tac	aaa	tac	ggc	aga	ggg	att	taa							2094
Val	Glu	Tyr	Lys	Tyr	Gly	Arg	Gly	Ile								
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 <212> PRT  
 <213> Neisseria meningitidis

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 Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg  
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09030433 081604

Leu	Leu	Phe	Ser	His	Ile	Gly	Ile	Asp	Leu	Ser	Ser	Ile	Thr	Val	Ile
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Ile	Ser	Val	Phe	Met	Val	Gly	Leu	Gly	Val	Gly	Ala	Tyr	Phe	Gly	Gly
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Arg	Ile	Ala	Asp	Arg	Phe	Pro	Ser	Ser	Ile	Ile	Pro	Leu	Phe	Cys	Ile
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Ala	Glu	Val	Ser	Ile	Gly	Leu	Phe	Gly	Leu	Val	Ser	Arg	Gly	Leu	Ile
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Ser	Gly	Leu	Gly	His	Leu	Leu	Val	Glu	Ala	Asp	Leu	Pro	Ile	Ile	Ala
		100						105				110			
Ala	Ala	Asn	Phe	Leu	Leu	Leu	Leu	Leu	Pro	Thr	Phe	Met	Met	Gly	Ala
		115				120						125			
Thr	Leu	Pro	Leu	Leu	Thr	Cys	Phe	Phe	Asn	Arg	Lys	Ile	His	Asn	Val
130						135						140			
Gly	Glu	Ser	Ile	Gly	Thr	Leu	Tyr	Phe	Phe	Asn	Thr	Leu	Gly	Ala	Ala
145				150						155				160	
Leu	Gly	Ser	Leu	Ala	Ala	Ala	Glu	Phe	Phe	Tyr	Val	Phe	Phe	Thr	Leu
				165				170						175	
Ser	Gln	Thr	Ile	Ala	Leu	Thr	Ala	Cys	Phe	Asn	Leu	Leu	Ile	Ala	Ala
		180						185				190			
Ser	Val	Cys	Cys	Val	Thr	Glu	Arg	Met	Asp	Ile	Val	Asn	Thr	Lys	Pro
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Asn	Thr	Ser	Leu	Ile	Tyr	Met	Leu	Ser	Phe	Leu	Ser	Gly	Leu	Leu	Ser
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Leu	Gly	Ile	Glu	Val	Leu	Trp	Val	Arg	Met	Phe	Ser	Phe	Ala	Ala	Gln
225				230						235				240	
Ser	Val	Pro	Gln	Ala	Phe	Ser	Phe	Thr	Leu	Ala	Tyr	Phe	Leu	Thr	Gly
				245				250						255	
Ile	Ala	Val	Gly	Ala	Tyr	Phe	Gly	Lys	Arg	Ile	Cys	Arg	Ser	Arg	Phe
		260						265				270			
Val	Asp	Ile	Pro	Phe	Ile	Gly	Gln	Cys	Phe	Leu	Trp	Ala	Gly	Ile	Ala
		275				280						285			
Asp	Phe	Leu	Ile	Leu	Gly	Ala	Ala	Trp	Leu	Leu	Thr	Gly	Phe	Ser	Gly
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Phe	Val	His	His	Ala	Gly	Ile	Phe	Ile	Thr	Leu	Ser	Ala	Val	Val	Arg
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Gly	Leu	Ile	Phe	Pro	Leu	Val	His	His	Val	Gly	Thr	Asp	Gly	Asn	Lys
				325				330						335	
Ser	Gly	Arg	Gln	Val	Ser	Asn	Val	Tyr	Phe	Ala	Asn	Val	Ala	Gly	Ser
		340						345				350			

Ala	Leu	Gly	Pro	Val	Leu	Ile	Gly	Phe	Val	Ile	Leu	Asp	Phe	Leu	Ser	355	360	365
Thr	Gln	Gln	Ile	Tyr	Leu	Leu	Ile	Cys	Leu	Ile	Ser	Ala	Ala	Val	Pro	370	375	380
Leu	Phe	Cys	Thr	Leu	Phe	Gln	Lys	Ser	Leu	Arg	Leu	Asn	Ala	Val	Ser	385	390	395
Val	Ala	Val	Ser	Leu	Met	Phe	Gly	Ile	Leu	Met	Phe	Leu	Leu	Pro	Asp	405	410	415
Ser	Val	Phe	Gln	Asn	Ile	Ala	Asp	Arg	Pro	Asp	Arg	Leu	Ile	Glu	Asn	420	425	430
Lys	His	Gly	Ile	Val	Ala	Val	Tyr	His	Arg	Asp	Gly	Asp	Lys	Val	Val	435	440	445
Tyr	Gly	Ala	Asn	Val	Tyr	Asp	Gly	Ala	Tyr	Asn	Thr	Asp	Val	Phe	Asn	450	455	460
Ser	Val	Asn	Gly	Ile	Glu	Arg	Ala	Tyr	Leu	Leu	Pro	Ser	Leu	Lys	Ser	465	470	475
Gly	Ile	Arg	Arg	Ile	Phe	Val	Val	Gly	Leu	Ser	Thr	Gly	Ser	Trp	Ala	485	490	495
Arg	Val	Leu	Ser	Ala	Ile	Pro	Glu	Met	Gln	Ser	Met	Ile	Val	Ala	Glu	500	505	510
Ile	Asn	Pro	Ala	Tyr	Arg	Ser	Leu	Ile	Ala	Asp	Glu	Pro	Gln	Ile	Ala	515	520	525
Pro	Leu	Leu	Gln	Asp	Lys	Arg	Val	Glu	Ile	Val	Leu	Asp	Asp	Gly	Arg	530	535	540
Lys	Trp	Leu	Arg	Arg	His	Pro	Asp	Glu	Lys	Phe	Asp	Leu	Ile	Leu	Met	545	550	555
Asn	Thr	Thr	Trp	Tyr	Trp	Arg	Ala	Tyr	Ser	Thr	Asn	Leu	Leu	Ser	Ala	565	570	575
Glu	Phe	Leu	Lys	Gln	Val	Gln	Ser	His	Leu	Thr	Pro	Asp	Gly	Ile	Val	580	585	590
Met	Phe	Asn	Thr	Thr	His	Ser	Pro	His	Ala	Phe	Ala	Thr	Ala	Val	His	595	600	605
Ser	Ile	Pro	Tyr	Ala	Tyr	Arg	Tyr	Gly	His	Met	Val	Val	Gly	Ser	Ala	610	615	620
Thr	Pro	Val	Val	Phe	Pro	Asn	Lys	Glu	Leu	Leu	Lys	Gln	Arg	Leu	Ser	625	630	635
Arg	Leu	Ile	Trp	Pro	Glu	Ser	Gly	Arg	His	Val	Phe	Asp	Ser	Ser	Thr	645	650	655
Val	Asp	Ala	Ala	Ala	Gln	Lys	Val	Val	Ser	Arg	Met	Leu	Ile	Gln	Met	660	665	670

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<213> Neisseria meningitidis

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Ala Val Ser Tyr Ala Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser  
35 40 45

Met Leu Cys Ala Gly Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala  
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Lys Ile Asn Ala Pro Pro Pro Asn Leu His Thr Gly Asp Phe Thr Asn  
65 70 75 80

Pro Asn Asp Ala Tyr Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu  
85 90 95

Ala Gly Tyr Thr Gly Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly  
100 105 110

Glu Ser Val Gly Ser Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu  
115 120 125

His Gly Tyr Asn Glu Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys  
130 135 140

Glu Ala Pro Glu Asp Gly Gly Gly Lys Asp Ile Lys Ala Ser Phe Asp  
145 150 155 160

Asp Glu Ala Val Ile Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His  
165 170 175

Val Lys Glu Ile Gly His Ile Asp Val Val Ser His Ile Ile Gly Gly  
180 185 190

Arg Ser Val Asp Gly Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr  
195 200 205

Leu His Ile Met Asn Thr His Asp Gly Thr Lys Asn Glu Ile Met Ser  
210 215 220

Ala Ala Ile Arg Asn Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg  
225 230 235 240

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Ile Val Asn Asn Ser Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp  
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His Phe Gln Ile Ala Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu  
260 265 270

Ala Tyr Ser Gly Gly Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln  
275 280 285

Gln Ser Asp Tyr Gly Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met  
290 295 300

Leu Phe Ile Phe Ser Ala Ser Asn Asp Ala Gln Ala Gln Pro Asn Thr  
305 310 315 320

Leu Thr Leu Leu Pro Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile  
325 330 335

Thr Val Ala Gly Val Asp Arg Ser Gly Glu Lys Phe Asn Gly Ser Asn  
340 345 350

His Cys Gly Ile Thr Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala  
355 360 365

Ser Val Arg Phe Thr Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser  
370 375 380

Phe Ser Ala Pro Ile Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys  
385 390 395 400

Tyr Pro Trp Met Ser Asn Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr  
405 410 415

Ala Gln Asp Ile Gly Ala Val Gly Val Asp Ser Lys Phe Gly Trp Gly  
420 425 430

Leu Leu Asp Ala Gly Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe  
435 440 445

Gly Asp Phe Thr Ala Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser  
450 455 460

Phe Arg Asn Asp Ile Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly  
465 470 475 480

Ser Gln Leu Gln Leu His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile  
485 490 495

Ile Glu Gly Gly Ser Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met  
500 505 510

Arg Val Glu Thr Lys Gly Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly  
515 520 525

Gly Ser Leu Asn Ser Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Arg  
530 535 540

Ser Gly Ala Asn Glu Thr Val His Ile Lys Gly Asp Leu Gln Leu Gly  
545 550 555 560

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Gly Glu Gly Thr Leu Tyr Thr Arg Leu Gly Lys Leu Leu Lys Val Asp  
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Gly Thr Ala Met Thr Gly Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys  
580 585 590

Gly Ala Gly Tyr Leu Asn Arg Thr Gly Gln Arg Val Pro Phe Leu Ser  
595 600 605

Ala Ala Lys Ile Gly Arg Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr  
610 615 620

Asp Gly Gly Leu Leu Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly  
625 630 635 640

Ser Glu Gly Asp Thr Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala  
645 650 655

Arg Thr Ala Ser Ala Ala Ala His Ser Ala Pro Ala Gly Leu Lys His  
660 665 670

Ala Val Glu Gln Gly Gly Ser Asn Leu Glu Asn Leu Met Val Glu Leu  
675 680 685

Asp Ala Ser Glu Ser Ser Ala Thr Pro Glu Thr Val Glu Thr Ala Ala  
690 695 700

Ala Asp Arg Thr Asp Met Pro Gly Ile Arg Pro Tyr Gly Ala Thr Phe  
705 710 715 720

Arg Ala Ala Ala Ala Val Gln His Ala Asn Ala Ala Asp Gly Val Arg  
725 730 735

Ile Phe Asn Ser Leu Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala  
740 745 750

His Ala Asp Met Gln Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu  
755 760 765

Asp His Asn Ala Thr Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp  
770 775 780

Gly Gly Thr Trp Glu Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser  
785 790 795 800

Thr Gln Thr Val Gly Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala  
805 810 815

Ala Ala Thr Leu Gly Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala  
820 825 830

Asn Ala Lys Thr Asp Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp  
835 840 845

Ala Gly Asp Ile Gly Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr  
850 855 860

Lys Asn Ser Ile Ser Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly  
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His	Leu	Gly	Val	Lys	Met	Tyr	Ser	His	Thr	Val	Pro	Ala	Ile	Ala	Glu	
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ttg	ata	gcg	aat	gcc	tac	gat	gca	tgt	gct	acg	gaa	gtg	gaa	gtt	agg	144
Leu	Ile	Ala	Asn	Ala	Tyr	Asp	Ala	Cys	Ala	Thr	Glu	Val	Glu	Val	Arg	
		35					40					45				
tta	ttc	gat	aaa	ccg	gag	cat	aaa	atc	gtt	att	aaa	gat	aat	ggc	ata	192
Leu	Phe	Asp	Lys	Pro	Glu	His	Lys	Ile	Val	Ile	Lys	Asp	Asn	Gly	Ile	
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Gly Met Ser Phe Asp Glu Ile Asn Asp Phe Tyr Leu Arg Ile Gly Arg	
65 70 75 80	
aac aga agg gaa gaa aaa caa gcc tcc ccg tgc gga aga att cca acg	288
Asn Arg Arg Glu Glu Lys Gln Ala Ser Pro Cys Gly Arg Ile Pro Thr	
85 90 95	
ggt aaa aaa ggt ctt ggt aaa ttg gca tta ttc agg ctt ggc aac aaa	336
Gly Lys Lys Gly Leu Gly Lys Leu Ala Leu Phe Arg Leu Gly Asn Lys	
100 105 110	
atc gaa atc tct act atc caa gga aac gaa cgg gtt act ttt act ttg	384
Ile Glu Ile Ser Thr Ile Gln Gly Asn Glu Arg Val Thr Phe Thr Leu	
115 120 125	
gat tat gca gag att aaa aaa agt gag cgt att tat caa ccg gag ttt	432
Asp Tyr Ala Glu Ile Lys Lys Ser Glu Arg Ile Tyr Gln Pro Glu Phe	
130 135 140	
cag aaa gag tct gtt aaa ccc aat acc gaa aac gga aca act ata act	480
Gln Lys Glu Ser Val Lys Pro Asn Thr Glu Asn Gly Thr Thr Ile Thr	
145 150 155 160	
tta acc gag ctg acg aaa aaa caa gga tac ccg tta gat aat tat gtg	528
Leu Thr Glu Leu Thr Lys Lys Gln Gly Tyr Pro Leu Asp Asn Tyr Val	
165 170 175	
ggg cat ctt tcc cgt tta ttt gat ttt ccg gct cag gat ttt aaa atc	576
Gly His Leu Ser Arg Leu Phe Asp Phe Pro Ala Gln Asp Phe Lys Ile	
180 185 190	
aaa gta agc ttg aac ggc tgc gaa cca aga atc att gac gga aac cta	624
Lys Val Ser Leu Asn Gly Ser Glu Pro Arg Ile Ile Asp Gly Asn Leu	
195 200 205	
aaa tat aat ctt gtt acc cca caa ttc gaa tgg gaa tac cag gat cta	672
Lys Tyr Asn Leu Val Thr Pro Gln Phe Glu Trp Glu Tyr Gln Asp Leu	
210 215 220	
gca acc aat att tca tgc tta tct tca aaa ttc gaa cag tat gaa tac	720
Ala Thr Asn Ile Ser Ser Leu Ser Ser Lys Phe Glu Gln Tyr Glu Tyr	
225 230 235 240	
agc gga tta ata caa ggt aag ttc att aca acg gaa aaa cct tta aag	768
Ser Gly Leu Ile Gln Gly Lys Phe Ile Thr Thr Glu Lys Pro Leu Lys	
245 250 255	
aat aat atg aaa ggt att acc ttg ttt gcc aac ggc aga atg gta aat	816
Asn Asn Met Lys Gly Ile Thr Leu Phe Ala Asn Gly Arg Met Val Asn	
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 <213> Neisseria gonorrhoeae

090433 084604

<400> 55

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Leu	Ile	Ala	Asn	Ala	Tyr	Asp	Ala	Cys	Ala	Thr	Glu	Val	Glu	Val	Arg
		35					40					45			
Leu	Phe	Asp	Lys	Pro	Glu	His	Lys	Ile	Val	Ile	Lys	Asp	Asn	Gly	Ile
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Gly	Met	Ser	Phe	Asp	Glu	Ile	Asn	Asp	Phe	Tyr	Leu	Arg	Ile	Gly	Arg
	65				70					75					80
Asn	Arg	Arg	Glu	Glu	Lys	Gln	Ala	Ser	Pro	Cys	Gly	Arg	Ile	Pro	Thr
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Gly	Lys	Lys	Gly	Leu	Gly	Lys	Leu	Ala	Leu	Phe	Arg	Leu	Gly	Asn	Lys
			100					105					110		
Ile	Glu	Ile	Ser	Thr	Ile	Gln	Gly	Asn	Glu	Arg	Val	Thr	Phe	Thr	Leu
		115					120					125			
Asp	Tyr	Ala	Glu	Ile	Lys	Lys	Ser	Glu	Arg	Ile	Tyr	Gln	Pro	Glu	Phe
	130					135					140				
Gln	Lys	Glu	Ser	Val	Lys	Pro	Asn	Thr	Glu	Asn	Gly	Thr	Thr	Ile	Thr
	145				150					155					160
Leu	Thr	Glu	Leu	Thr	Lys	Lys	Gln	Gly	Tyr	Pro	Leu	Asp	Asn	Tyr	Val
				165					170					175	
Gly	His	Leu	Ser	Arg	Leu	Phe	Asp	Phe	Pro	Ala	Gln	Asp	Phe	Lys	Ile
			180					185					190		
Lys	Val	Ser	Leu	Asn	Gly	Ser	Glu	Pro	Arg	Ile	Ile	Asp	Gly	Asn	Leu
		195					200					205			
Lys	Tyr	Asn	Leu	Val	Thr	Pro	Gln	Phe	Glu	Trp	Glu	Tyr	Gln	Asp	Leu
	210					215					220				
Ala	Thr	Asn	Ile	Ser	Ser	Leu	Ser	Ser	Lys	Phe	Glu	Gln	Tyr	Glu	Tyr
	225				230					235					240
Ser	Gly	Leu	Ile	Gln	Gly	Lys	Phe	Ile	Thr	Thr	Glu	Lys	Pro	Leu	Lys
				245					250					255	
Asn	Asn	Met	Lys	Gly	Ile	Thr	Leu	Phe	Ala	Asn	Gly	Arg	Met	Val	Asn
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<212> DNA

<213> Neisseria gonorrhoeae

0930433-084604

$\langle 222 \rangle \quad (1) \dots (1572)$ 

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Leu Ser Lys Ile Pro Val Phe Lys Gln Pro Ala Pro Ser Lys Ile Gly

195	200	205	
caa ggc agt att caa aat atc gtc ctg att atg ggc gaa agc gaa agc Gln Gly Ser Ile Gln Asn Ile Val Leu Ile Met Gly Glu Ser Glu Ser 210 215 220			672
gcg gcg cat ttg aaa ttg ttt ggt tac ggg cgc gaa act tcg ccg ttt Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe 225 230 240			720
tta acc cgg ctg tcg caa gcc gat ttt aag ccg att gtg aaa caa agt Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser 245 250 255			768
tat tcc gca ggc ttt atg acg gca gta tcc ctg ccc agt ttc ttt aac Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn 260 265 270			816
gtc ata ccg cac gcc aac ggc ttg gaa caa atc agc ggc ggc gat acc Val Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr 275 280 285			864
aat atg ttc cgc ctc gcc aaa gag cag ggc tat gaa acg tat ttt tac Asn Met Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr 290 295 300			912
agt gcc cag gct gaa aac caa atg gca att ttg aac tta atc ggt aag Ser Ala Gln Ala Glu Asn Gln Met Ala Ile Leu Asn Leu Ile Gly Lys 305 310 315 320			960
aaa tgg ata gac cat ctg att cag ccg acg caa ctt ggc tac ggc aac Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn 325 330 335			1008
ggc gac aat atg ccc gat gag aag ctg ctg ccg ttg ttc gac aaa atc Gly Asp Asn Met Pro Asp Glu Lys Leu Leu Pro Leu Phe Asp Lys Ile 340 345 350			1056
aat ttg cag cag ggc agg cat ttt atc gtg ttg cac caa cgc ggt tcg Asn Leu Gln Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser 355 360 365			1104
cac gcc cca tac ggc gca ttg ttg cag cct caa gat aaa gta ttc ggc His Ala Pro Tyr Gly Ala Leu Leu Gln Pro Gln Asp Lys Val Phe Gly 370 375 380			1152
gaa gcc gat att gtg gat aag tac gac aac acc atc cac aaa acc gac Glu Ala Asp Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp 385 390 395 400			1200
caa atg att caa acc gta ttc gag cag ctg caa aag cag cct gac ggc Gln Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly 405 410 415			1248
aac tgg ctg ttt gcc tat acc tcc gat cat ggc cag tat gtg cgc caa Asn Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln 420 425 430			1296
gat atc tac aat caa ggc acg gtg cag ccc gac agc tat att gtg cct Asp Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Ile Val Pro 435 440 445			1344

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435	440	445	
ctg gtt ttg tac agc ccg gat aag gcc gtg caa cag gct gcc aac cag			1392
Leu Val Leu Tyr Ser Pro Asp Lys Ala Val Gln Gln Ala Ala Asn Gln			
450	455	460	
gct ttt gcg cct tgc gag att gcc ttc cat cag cag ctt tca acg ttc			1440
Ala Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe			
465	470	475	480
ctg att cac acg ttg ggc tac gat atg ccg gtt tca ggt tgt cgc gaa			1488
Leu Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu			
	485	490	495
ggc tcg gta aca ggc aac ctg att acg gcc gat gca gcc agc ttg aac			1536
Gly Ser Val Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn			
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 Ala Ala Lys Met Ala Glu Thr Phe Ala Leu Thr Phe Met Ile Ala Ala  
 35 40 45  
 Leu Tyr Leu Phe Ala Arg Tyr Lys Ala Ser Arg Leu Leu Ile Ala Val  
 50 55 60  
 Phe Phe Ala Phe Ser Met Ile Ala Asn Asn Val His Tyr Ala Val Tyr  
 65 70 75 80  
 Gln Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Val  
 85 90 95  
 Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu  
 100 105 110  
 Pro Ala Leu Trp Gly Val Ala Glu Val Met Leu Phe Cys Ser Leu Ala  
 115 120 125  
 Lys Phe Arg Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe  
 130 135 140  
 Leu Met Leu Met Ile Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His  
 145 150 155 160  
 Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe

00800433 001604

	165		170		175
Ser Phe Gly Tyr Phe Val Gly Arg Val Leu Pro Tyr Gln Leu Phe Asp	180		185		190
Leu Ser Lys Ile Pro Val Phe Lys Gln Pro Ala Pro Ser Lys Ile Gly	195		200		205
Gln Gly Ser Ile Gln Asn Ile Val Leu Ile Met Gly Glu Ser Glu Ser	210		215		220
Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe	225		230		235
Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser	245		250		255
Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn	260		265		270
Val Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr	275		280		285
Asn Met Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr	290		295		300
Ser Ala Gln Ala Glu Asn Gln Met Ala Ile Leu Asn Leu Ile Gly Lys	305		310		315
Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn	325		330		335
Gly Asp Asn Met Pro Asp Glu Lys Leu Leu Pro Leu Phe Asp Lys Ile	340		345		350
Asn Leu Gln Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser	355		360		365
His Ala Pro Tyr Gly Ala Leu Leu Gln Pro Gln Asp Lys Val Phe Gly	370		375		380
Glu Ala Asp Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp	385		390		395
Gln Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly	405		410		415
Asn Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln	420		425		430
Asp Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Ile Val Pro	435		440		445
Leu Val Leu Tyr Ser Pro Asp Lys Ala Val Gln Gln Ala Ala Asn Gln	450		455		460
Ala Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe	465		470		475
Leu Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu					480

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485

490

495

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Ile Arg Asn Gly Lys Ala Glu Tyr Val Tyr Pro Gln  
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<213> Neisseria gonorrhoeae

<220>

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1 5 10 15

ttg ctg acg gaa aaa gtg tgg ccc atc atc gca tta atc ttg gtg ccg 96  
Leu Leu Thr Glu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro  
20 25 30

ctg att ggg gcg ttg ctg ggg ggg ttt gat gta tcc caa tta aaa gaa 144  
Leu Ile Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu  
35 40 45

ttt tat tgg ggc ggc acg aaa tgg gtg acg cag att gtg att atg ttt 192  
Phe Tyr Ser Gly Gly Thr Lys Ser Val Thr Gln Ile Val Ile Met Phe  
50 55 60

atg ttt tcc att ttg ttt ttt gga atc atg aac gat gtg ggg ctg ttc 240  
Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe  
65 70 75 80

cgt ccg atg ata ggc ggt ttg att aag ctg act cgg ggt aat atc gtg 288  
Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val  
85 90 95

gca gtg agt gtg ggg acg gtc ttg gtg tgg gtg gca cag ttg gac 336  
Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp  
100 105 110

ggg gcg ggc gcg acg acg ttt tta tgg gtc gtc ccc gcc ctt ttg ccg 384  
Gly Ala Gly Ala Thr Thr Phe Leu Ser Val Val Pro Ala Leu Leu Pro  
115 120 125

ctt tac aag cgt ctg cat atg aat cct tac ctg ctg ttt ttg ctg ctg 432  
Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu  
130 135 140

act tcc agc gcg ggg cta atc aac ctt ttg ccg cgg ggc ggg ccg atc 480  
Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Arg Gly Gly Pro Ile  
145 150 155 160

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ggg	cgg	gtt	gca	agc	gtg	ttg	ggc	gca	gat	gtg	ggc	gaa	ttg	tat	aaa	528
Gly	Arg	Val	Ala	Ser	Val	Leu	Gly	Ala	Asp	Val	Gly	Glu	Leu	Tyr	Lys	
				165						170				175		
cct	ttg	ttg	acg	gtg	caa	att	atc	ggc	gtg	gtg	ttt	atc	ctt	gtg	ctg	576
Pro	Leu	Leu	Thr	Val	Gln	Ile	Ile	Gly	Val	Val	Phe	Ile	Leu	Val	Leu	
			180					185					190			
tcc	ctg	ttt	ttg	ggc	gtg	cgt	gaa	aaa	agg	cgg	att	gtc	cgg	gag	ttg	624
Ser	Leu	Phe	Leu	Gly	Val	Arg	Glu	Lys	Arg	Arg	Ile	Val	Arg	Glu	Leu	
		195					200					205				
ggc	gcg	ttg	ccc	gcc	gtg	ggc	gat	ttg	ata	aag	cgc	gcg	cct	ttg	tcg	672
Gly	Ala	Leu	Pro	Ala	Val	Ala	Asp	Leu	Ile	Lys	Pro	Ala	Pro	Leu	Ser	
		210				215					220					
gaa	gaa	gaa	caa	aaa	ttg	ggc	cgt	cgc	aaa	ctg	ttt	tgg	tgg	aat	gtc	720
Glu	Glu	Glu	Gln	Lys	Leu	Ala	Arg	Pro	Lys	Leu	Phe	Trp	Trp	Asn	Val	
225					230					235					240	
ctg	ctg	ttt	ttg	ggc	ggc	atg	agc	ctg	ctt	ttt	tcg	ggc	atc	ttc	cgc	768
Leu	Leu	Phe	Leu	Ala	Ala	Met	Ser	Leu	Leu	Phe	Ser	Gly	Ile	Phe	Pro	
				245					250					255		
cgc	ggc	tat	gta	ttt	atg	ctg	gct	gta	acg	ggc	ggc	ttg	ctt	ttg	aat	816
Pro	Gly	Tyr	Val	Phe	Met	Leu	Ala	Ala	Thr	Ala	Ala	Leu	Leu	Leu	Asn	
			260					265					270			
tac	cgc	agc	cgc	cag	gaa	cag	atg	gag	cgg	att	tat	gcc	cac	gcc	ggc	864
Tyr	Arg	Ser	Pro	Gln	Glu	Gln	Met	Glu	Arg	Ile	Tyr	Ala	His	Ala	Gly	
		275					280					285				
ggc	gcg	gtg	atg	atg	ggc	tcc	att	atc	ttg	ggc	gca	ggc	acg	ttc	ttg	912
Gly	Ala	Val	Met	Met	Ala	Ser	Ile	Ile	Leu	Ala	Ala	Gly	Thr	Phe	Leu	
	290					295					300					
ggg	att	ttg	aag	ggc	ggc	ggg	atg	ttg	gac	ggc	att	tcc	aaa	gac	ctt	960
Gly	Ile	Leu	Lys	Gly	Ala	Gly	Met	Leu	Asp	Ala	Ile	Ser	Lys	Asp	Leu	
305					310					315					320	
gtg	cat	atc	ctg	cgc	gac	ggc	ttg	ctg	cct	tat	ctg	cat	att	gcc	atc	1008
Val	His	Ile	Leu	Pro	Asp	Ala	Leu	Leu	Pro	Tyr	Leu	His	Ile	Ala	Ile	
				325					330					335		
ggc	gtg	ttg	ggc	att	cgc	ctt	gag	ttg	gtc	ttg	agc	acg	gac	gct	tat	1056
Gly	Val	Leu	Gly	Ile	Pro	Leu	Glu	Leu	Val	Leu	Ser	Thr	Asp	Ala	Tyr	
			340				345						350			
tat	ttc	gga	ctg	ttt	cgc	att	gtg	gaa	cag	att	acc	tcg	cag	ggc	ggc	1104
Tyr	Phe	Gly	Leu	Phe	Pro	Ile	Val	Glu	Gln	Ile	Thr	Ser	Gln	Ala	Gly	
		355														

ttg gcg aaa ttg tgc atg ggc aaa cac atc cgt tat tgc ttt ttc tgg 1248  
 Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp  
                     405                    410                    415

gcg tgg ggt ttg tgc ctg gcg ata ttg gtc agt tgc ata gcg gca gga 1296  
 Ala Trp Gly Leu Ser Leu Ala Ile Leu Val Ser Ser Ile Ala Ala Gly  
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atc gtc cct ctg ccg taa 1314  
 Ile Val Pro Leu Pro  
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 <212> PRT  
 <213> Neisseria gonorrhoeae

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                     20                    25                    30

Leu Ile Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu  
                     35                    40                    45

Phe Tyr Ser Gly Gly Thr Lys Ser Val Thr Gln Ile Val Ile Met Phe  
                     50                    55                    60

Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe  
                     65                    70                    75                    80

Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val  
                     85                    90                    95

Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp  
                     100                    105                    110

Gly Ala Gly Ala Thr Thr Phe Leu Ser Val Val Pro Ala Leu Leu Pro  
                     115                    120                    125

Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu  
                     130                    135                    140

Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Arg Gly Gly Pro Ile  
                     145                    150                    155                    160

Gly Arg Val Ala Ser Val Leu Gly Ala Asp Val Gly Glu Leu Tyr Lys  
                     165                    170                    175

Pro Leu Leu Thr Val Gln Ile Ile Gly Val Val Phe Ile Leu Val Leu  
                     180                    185                    190

Ser Leu Phe Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu  
                     195                    200                    205

Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Ala Pro Leu Ser  
                     210                    215                    220

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Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val  
 225 230 235 240

Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro  
 245 250 255

Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Leu Asn  
 260 265 270

Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly  
 275 280 285

Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu  
 290 295 300

Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Leu  
 305 310 315 320

Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile  
 325 330 335

Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr  
 340 345 350

Tyr Phe Gly Leu Phe Pro Ile Val Glu Gln Ile Thr Ser Gln Ala Gly  
 355 360 365

Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val  
 370 375 380

Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly  
 385 390 395 400

Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp  
 405 410 415

Ala Trp Gly Leu Ser Leu Ala Ile Leu Val Ser Ser Ile Ala Ala Gly  
 420 425 430

Ile Val Pro Leu Pro  
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 1 5 10 15  
 act tat ctg tat caa aag ccc aag ctc ttc aaa gga gcg gtt cgg aat 96

0030433 DB1601

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			20					25					30			
ctc	gaa	gcc	gca	tct	tgt	aaa	tat	atc	aac	gag	ata	tac	caa	cga	gca	144
Leu	Glu	Ala	Ala	Ser	Cys	Lys	Tyr	Ile	Asn	Glu	Ile	Tyr	Gln	Arg	Ala	
		35					40					45				
gac	cca	acc	gca	ccg	ctg	ttt	cat	ctg	cgt	aaa	aaa	ggc	gca	atc	ggt	192
Asp	Pro	Thr	Ala	Pro	Leu	Phe	His	Leu	Arg	Lys	Lys	Gly	Ala	Ile	Val	
	50					55					60					
ccg	aaa	gaa	gaa	tac	gtc	gaa	agt	ttc	gac	gat	ttg	ggc	aaa	act	cgc	240
Pro	Lys	Glu	Glu	Tyr	Val	Glu	Ser	Phe	Asp	Asp	Leu	Gly	Lys	Thr	Arg	
	65				70				75						80	
tac	cgt	ttt	att	aaa	tcc	gtt	atc	tac	gaa	cat	atg	aag	aat	ggg	gcg	288
Tyr	Arg	Phe	Ile	Lys	Ser	Val	Ile	Tyr	Glu	His	Met	Lys	Asn	Gly	Ala	
				85				90						95		
tcg	tta	gtc	tat	aac	cat	att	aac	aac	gag	ccg	ttt	tca	gac	cat	atc	336
Ser	Leu	Val	Tyr	Asn	His	Ile	Asn	Asn	Glu	Pro	Phe	Ser	Asp	His	Ile	
			100					105					110			
gcc	cgt	caa	gtc	gcc	cgc	ttt	gcc	ggc	gca	cat	act	att	gtt	agt	gga	384
Ala	Arg	Gln	Val	Ala	Arg	Phe	Ala	Gly	Ala	His	Thr	Ile	Val	Ser	Gly	
		115					120					125				
tat	ctt	gct	ttt	ggc	agc	gac	gaa	tct	tat	aaa	aac	cat	tgg	gat	acc	432
Tyr	Leu	Ala	Phe	Gly	Ser	Asp	Glu	Ser	Tyr	Lys	Asn	His	Trp	Asp	Thr	
	130				135						140					
cgc	gat	gtg	tat	gcc	atc	cag	ctt	ttc	ggc	aag	aaa	cgt	tgg	caa	ctt	480
Arg	Asp	Val	Tyr	Ala	Ile	Gln	Leu	Phe	Gly	Lys	Lys	Arg	Trp	Gln	Leu	
	145				150					155					160	
act	gcc	cct	gat	ttc	cct	atg	cca	ttg	tat	atg	caa	cag	act	aaa	gat	528
Thr	Ala	Pro	Asp	Phe	Pro	Met	Pro	Leu	Tyr	Met	Gln	Gln	Thr	Lys	Asp	
				165				170					175			
act	gat	att	tcc	att	cct	gaa	cat	atc	gat	atg	gat	att	atc	ctt	gaa	576
Thr	Asp	Ile	Ser	Ile	Pro	Glu	His	Ile	Asp	Met	Asp	Ile	Ile	Leu	Glu	
			180					185					190			
gca	ggg	gat	gtc	ctc	tac	atc	cca	cgc	ggg	tgg	tgg	cac	aga	cct	atc	624
Ala	Gly	Asp	Val	Leu	Tyr	Ile	Pro	Arg	Gly	Trp	Trp	His	Arg	Pro	Ile	
		195					200					205				
ccg	ctc	ggc	tgt	gaa	acc	ttc	cac	ttc	gct	gtc	ggg	acc	ttc	cca	cca	672
Pro	Leu	Gly	Cys	Glu	Thr	Phe	His	Phe	Ala	Val	Gly	Thr	Phe	Pro	Pro	
	210					215					220					
aac	ggc	tat	aat	tac	ctc	gag	tgg	cta	atg	aag	aaa	ttt	ccc	acc	ata	720
Asn	Gly	Tyr	Asn	Tyr	Leu	Glu	Trp	Leu	Met	Lys	Lys	Phe	Pro	Thr	Ile	
	225				230				235						240	
gaa	agt	ctg	cgc	cac	agt	ttc	tca	gac	tgg	gag	caa	gat	agg	acg	cgt	768
Glu	Ser	Leu	Arg	His	Ser	Phe	Ser	Asp	Trp	Glu	Gln	Asp	Arg	Thr	Arg	
				245				250					255			
atc	aac	gat	act	gcc	gca	caa	att	gct	gcc	atg	att	gcc	gac	ccc	gtc	816

05030433-081501

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<210> 61
<211> 384
<212> PRT
<213> Neisseria gonorrhoeae
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  1                      5                      10                      15

Thr Tyr Leu Tyr Gln Lys Pro Lys Leu Phe Lys Gly Ala Val Arg Asn
                20                      25                      30

Leu Glu Ala Ala Ser Cys Lys Tyr Ile Asn Glu Ile Tyr Gln Arg Ala
          35                      40                      45

Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val
      50                      55                      60

Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg
  65                      70                      75                      80

Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala
                85                      90                      95

Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile
          100                      105                      110

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Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly  
115 120 125

Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr  
130 135 140

Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu  
145 150 155 160

Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp  
165 170 175

Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu  
180 185 190

Ala Gly Asp Val Leu Tyr Ile Pro Arg Gly Trp Trp His Arg Pro Ile  
195 200 205

Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro  
210 215 220

Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile  
225 230 235 240

Glu Ser Leu Arg His Ser Phe Ser Asp Trp Glu Gln Asp Arg Thr Arg  
245 250 255

Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val  
260 265 270

Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp  
275 280 285

Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu  
290 295 300

Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu  
305 310 315 320

Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu  
325 330 335

Leu Gly Lys Lys Val Leu Glu His Ile Gly Lys Asn Glu Pro Leu Leu  
340 345 350

Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Ala Lys His Glu Glu Val  
355 360 365

Arg Lys Leu Ile Tyr Gln Leu Ile Glu Leu Asp Phe Leu Glu Ile Leu  
370 375 380

<210> 62  
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<212> DNA  
<213> Neisseria meningitidis

<220>

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Met	Asn	Arg	Pro	Lys	Gln	Pro	Phe	Phe	Arg	Pro	Glu	Val	Ala	Val	Ala	
1				5					10					15		
cgc	caa	acc	agc	ctg	acg	ggg	aaa	gtg	att	ctg	aca	cga	ccg	ttg	tca	96
Arg	Gln	Thr	Ser	Leu	Thr	Gly	Lys	Val	Ile	Leu	Thr	Arg	Pro	Leu	Ser	
			20					25					30			
ttt	tcc	cta	tgg	acg	aca	ttt	gca	tcg	ata	tct	gcg	tta	ttg	att	atc	144
Phe	Ser	Leu	Trp	Thr	Thr	Phe	Ala	Ser	Ile	Ser	Ala	Leu	Leu	Ile	Ile	
		35					40					45				
ctg	ttt	ttg	ata	ttt	ggg	aac	tat	acg	cga	aag	aca	aca	gtg	gag	gga	192
Leu	Phe	Leu	Ile	Phe	Gly	Asn	Tyr	Thr	Arg	Lys	Thr	Thr	Val	Glu	Gly	
		50				55					60					
caa	att	tta	cct	gca	tcg	ggc	gta	atc	agg	gtg	tat	gca	ccg	gat	acg	240
Gln	Ile	Leu	Pro	Ala	Ser	Gly	Val	Ile	Arg	Val	Tyr	Ala	Pro	Asp	Thr	
65					70				75					80		
ggg	aca	att	aca	gcg	aaa	ttc	gtg	gaa	gat	gga	gaa	aag	gtt	aag	gct	288
Gly	Thr	Ile	Thr	Ala	Lys	Phe	Val	Glu	Asp	Gly	Glu	Lys	Val	Lys	Ala	
				85					90					95		
ggc	gac	aag	cta	ttt	gcg	ctt	tcg	acc	tca	cgt	ttc	ggc	gca	gga	gat	336
Gly	Asp	Lys	Leu	Phe	Ala	Leu	Ser	Thr	Ser	Arg	Phe	Gly	Ala	Gly	Asp	
			100					105					110			
agc	gtg	cag	cag	cag	ctg	aaa	acg	gag	gca	gtt	ctg	aag	aaa	acg	ttg	384
Ser	Val	Gln	Gln	Gln	Leu	Lys	Thr	Glu	Ala	Val	Leu	Lys	Lys	Thr	Leu	
		115					120					125				
gca	gaa	cag	gaa	ctg	ggg	cgt	ctg	aag	ctg	ata	cac	ggg	aat	gaa	acg	432
Ala	Glu	Gln	Glu	Leu	Gly	Arg	Leu	Lys	Leu	Ile	His	Gly	Asn	Glu	Thr	
		130				135					140					
cgc	agc	ctt	aaa	gca	act	gtc	gaa	cgt	ttg	gaa	aac	cag	gaa	ctc	cat	480
Arg	Ser	Leu	Lys	Ala	Thr	Val	Glu	Arg	Leu	Glu	Asn	Gln	Glu	Leu	His	
145					150					155				160		
att	tcg	caa	cag	ata	gac	ggg	cag	aaa	agg	cgc	att	aga	ctt	gcg	gaa	528
Ile	Ser	Gln	Gln	Ile	Asp	Gly	Gln	Lys	Arg	Arg	Ile	Arg	Leu	Ala	Glu	
				165					170					175		
gaa	atg	ttg	cag	aaa	tat	cgt	ttc	cta	tcc	gcc	aat	gat	gca	gtg	cca	576
Glu	Met	Leu	Gln	Lys	Tyr	Arg	Phe	Leu	Ser	Ala	Asn	Asp	Ala	Val	Pro	
			180					185					190			
aaa	caa	gaa	atg	atg	aat	gtc	aag	gca	gag	ctt	tta	gag	cag	aaa	gcc	624
Lys	Gln	Glu	Met	Met	Asn	Val	Lys	Ala	Glu	Leu	Leu	Glu	Gln	Lys	Ala	
		195					200					205				
aaa																

<210> 63

<213> Neisseria meningitidis

Arg Thr Gln Asn Leu Thr Leu Ala Ser Leu Pro Gln Ala Ala  
225 230 235

<213> Neisseria meningitidis

<220>

$\langle 222 \rangle \quad (1) \dots (687)$ 

atg	atg	aat	gtc	gag	gag	gca	gag	ctt	tta	gag	cag	aaa	gcc	aaa	ctt	gat	48
Met	Met	Asn	Val	Glu	Ala	Glu	Leu	Leu	Glu	Gln	Lys	Ala	Lys	Leu	Asp		
1			5						10						15		
gcc	tac	ggc	cga	gaa	gaa	gcc	ggg	ctg	ctt	cag	gaa	atc	cgc	acg	cag	96	
Ala	Tyr	Gly	Arg	Glu	Glu	Ala	Gly	Leu	Leu	Gln	Glu	Ile	Arg	Thr	Gln		
		20					25						30				
aat	ctg	aca	ttg	gcc	agc	ctc	ccc	aaa	cgg	cat	gag	aca	gaa	caa	agc	144	
Asn	Leu	Thr	Leu	Ala	Ser	Leu	Pro	Lys	Arg	His	Glu	Thr	Glu	Gln	Ser		
	35					40						45					
cag	ctt	gaa	cgc	acc	atg	gcc	gat	att	tct	caa	gaa	gtt	ttg	gat	ttt	192	
Gln	Leu	Glu	Arg	Thr	Met	Ala	Asp	Ile	Ser	Gln	Glu	Val	Leu	Asp	Phe		
50					55					60							
gaa	atg	cgc	tct	gaa	caa	atc	atc	cgt	gca	gga	cgg	tcg	ggc	tat	ata	240	
Glu	Met	Arg	Ser	Glu	Gln	Ile	Ile	Arg	Ala	Gly	Arg	Ser	Gly	Tyr	Ile		
65				70					75					80			
gca	ata	ccg	aac	gtc	gaa	gtc	gga	cgg	cag	gtt	gat	cct	tcc	aaa	ctg	288	
Ala	Ile	Pro	Asn	Val	Glu	Val	Gly	Arg	Gln	Val	Asp	Pro	Ser	Lys	Leu		
			85					90						95			
ctc	ttg	agc	att	gtt	ccc	gaa	cgt	acc	gag	tta	tat	goc	cat	cta	tat	336	
Leu	Leu	Ser	Ile	Val	Pro	Glu	Arg	Thr	Glu	Leu	Tyr	Ala	His	Leu	Tyr		
		100					105						110				
atc	ccc	agc	agt	gca	gca	ggc	ttc	atc	aag	ccg	aaa	gac	aag	gtt	gtc	384	
Ile	Pro	Ser	Ser	Ala	Ala	Gly	Phe	Ile	Lys	Pro	Lys	Asp	Lys	Val	Val		
	115					120						125					
cta	cgt	tat	cag	gca	tat	ccc	tat	cag	aaa	ttc	ggg	ctt	gct	tcc	ggc	432	
Leu	Arg	Tyr	Gln	Ala	Tyr	Pro	Tyr	Gln	Lys	Phe	Gly	Leu	Ala	Ser	Gly		
	130					135					140						
agt	gtc	gta	tca	gtg	gca	aaa	acg	gca	ctg	ggc	aga	cag	gaa	ttg	tcg	480	
Ser	Val	Val	Ser	Val	Ala	Lys	Thr	Ala	Leu	Gly	Arg	Gln	Glu	Leu	Ser		
145				150					155					160			
gga	ttg	ggc	atg	gta	tcc	tcc	gat	ttg	goc	aag	agc	aac	gaa	cct	gtt	528	
Gly	Leu	Gly	Met	Val	Ser	Ser	Asp	Leu	Ala	Lys	Ser	Asn	Glu	Pro	Val		
			165					170						175			
tat	ctc	gtg	aaa	ata	aaa	ccc	gac	aaa	cca	acc	atc	act	gca	tac	ggc	576	
Tyr	Leu	Val	Lys	Ile	Lys	Pro	Asp	Lys	Pro	Thr	Ile	Thr	Ala	Tyr	Gly		
			180					185					190				
gag	gaa	aaa	ccg	ctg	caa	atc	ggc	atg	acg	ctg	gaa	gca	gac	atc	cta	624	
Glu	Glu	Lys	Pro	Leu	Gln	Ile	Gly	Met	Thr	Leu	Glu	Ala	Asp	Ile	Leu		

<210> 65  
 <211> 229  
 <212> PRT  
 <213> Neisseria gonorrhoeae

<400> 65  
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 Ala Tyr Gly Arg Glu Glu Ala Gly Leu Leu Gln Glu Ile Arg Thr Gln  
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 Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser  
 35 40 45  
 Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe  
 50 55 60  
 Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile  
 65 70 75 80  
 Ala Ile Pro Asn Val Glu Val Gly Arg Gln Val Asp Pro Ser Lys Leu  
 85 90 95  
 Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr  
 100 105 110  
 Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val  
 115 120 125  
 Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly  
 130 135 140  
 Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser  
 145 150 155 160  
 Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val  
 165 170 175  
 Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly  
 180 185 190  
 Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu  
 195 200 205  
 His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Pro Ile Tyr Ser  
 210 215 220  
 Met Ser Gly Arg Leu  
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<210> 66  
 <211> 924  
 <212> DNA  
 <213> Neisseria gonorrhoeae

<220>

09830433 081604

$\langle 222 \rangle \quad (1) \dots (921)$ 

<400> 66

atg caa tac agc aca ctg gca gga caa acc gac aac tcc ctc gtt tcc 48  
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1 5 10 15

aat aat ttc ggg ttt ttg cgc ctg cgg ctt aat ttt atg ccg tat gaa 96  
Asn Asn Phe Gly Phe Leu Arg Leu Pro Leu Asn Phe Met Pro Tyr Glu  
20 25 30

agc cat gcc gat tgg gtt att acc ggc gtg cct tat gat atg gcg gtt 144  
 Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val  
           35                          40                          45

tca ggg cgt tcc ggc ggc cgt ttc ggt cct gaa gcc atc cgg cgc gcc 192  
Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala  
50 55 60

tcc gtc aac ctc gct tgg gag cac cgc agg ttt ccg tgg aca ttt gat 240  
 Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp  
 65 70 75 80

gtg cgc gaa cgc ctg aac att att gat tgc ggc gac ttg gtt ttt tct 288  
Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser  
85 90 95

ttt ggc gac agc agg gat ttt gtc gaa aaa atg gaa ggg cac gcc gcc 336  
Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly  
100 105 110

aaa tta ctt tct ttc ggc aaa cgc tgt ttg agt ttg ggc ggc gac cat 384  
Lys Leu Leu Ser Phe Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His  
115 120 125

ttc att acc ctc cgg ttg ttg cgc gcc cac gcc cgc tat ttc ggc aaa 432  
Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys  
130 135 140

ctc gca ctg att cat ttt gac ggc cac acc gac acc tac gac aac ggc 480  
Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly  
143 150 155 160

agc gaa tac gac cac gcc acg atg ttt tat acc gcc ccc aag gaa gcc      528  
Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly  
                165                         170                         175

ctc atc gac cgc tcc cgt tcc gta caa atc ggc ata cgc acc gaa cac 576  
Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His  
180 185 190

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agt aaa aaa ttg cct ttt act gtg ttg tcc gcc ccc aaa gtc aat gaa 624
Ser Lys Lys Leu Pro Phe Thr Val Leu Ser Ala Pro Lys Val Asn Glu
    195                                200                                205

gac agt gtt gaa gag acc gtc cgt aaa atc aaa gaa acc gtc ggc aat 672
Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn
    210                                215                                220

atg ccc gtt tac ctg act ttc gac ata gac tgt ctc gac ccg tcg ttc 720
Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe
    225                                230                                235                                240

gcc ccc ggg acc ggt acg ccc gta tgc ggc ggc ttg agc agc gac agg 768
Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg
    245                                250                                255

gca tta aaa atc cta cgt ggg ctg acg gat ctc gac atc gtc ggt atg 816
Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met
    260                                265                                270

gat gtt gta gaa gtt gcc ccc tct tac gac caa tcc gac att acc gct 864
Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala
    275                                280                                285

ttg gcc ggc gcc aca att gcc ttg gaa atg ctt tac ctt caa ggt gcg 912
Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Gln Gly Ala
    290                                295                                300

aaa aaq gac tga
Lys Lys Asp
305

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<210> 67  
 <211> 307  
 <212> PRT  
 <213> Neisseria gonorrhoeae

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<400> 67
Met Gln Tyr Ser Thr Leu Ala Gly Gln Thr Asp Asn Ser Leu Val Ser
  1                                5                                10                                15

Asn Asn Phe Gly Phe Leu Arg Leu Pro Leu Asn Phe Met Pro Tyr Glu
    20                                25                                30

Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val
    35                                40                                45

Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala
    50                                55                                60

Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp
    65                                70                                75                                80

Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser
    85                                90                                95

Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly
    100                                105                                110

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109190"EEH0E360

Lys Leu Leu Ser Phe Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His  
 115 120 125

Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys  
 130 135 140

Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly  
 145 150 155 160

Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly  
 165 170 175

Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His  
 180 185 190

Ser Lys Lys Leu Pro Phe Thr Val Leu Ser Ala Pro Lys Val Asn Glu  
 195 200 205

Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn  
 210 215 220

Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe  
 225 230 235 240

Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg  
 245 250 255

Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met  
 260 265 270

Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala  
 275 280 285

Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Gln Gly Ala  
 290 295 300

Lys Lys Asp  
 305

<210> 68  
 <211> 1404  
 <212> DNA  
 <213> Neisseria meningitidis

<220>  
 <221> CDS  
 <222> (1)..(1401)

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 Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val  
 1 5 10 15

tgc ctg aca ctg acg ccc tat ttg caa cat gaa cta ttt tgg gct atg 96  
 Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met  
 20 25 30

aaa tcc tat ttt tcc aaa tat atc cta ccc gtt tca ctt ttt acc ttg 144

0930433 081604

Lys	Ser	Tyr	Phe	Ser	Lys	Tyr	Ile	Leu	Pro	Val	Ser	Leu	Phe	Thr	Leu	
		35					40					45				
cca	cta	tcc	ctt	tcc	cca	tcc	gtt	tcg	gct	ttt	acg	ctg	cct	gaa	gca	192
Pro	Leu	Ser	Leu	Ser	Pro	Ser	Val	Ser	Ala	Phe	Thr	Leu	Pro	Glu	Ala	
	50					55					60					
tgg	cgg	gcg	gcg	cag	caa	cat	tcg	gct	gat	ttt	caa	gcg	tcc	cat	tac	240
Trp	Arg	Ala	Ala	Gln	Gln	His	Ser	Ala	Asp	Phe	Gln	Ala	Ser	His	Tyr	
	65				70					75					80	
cag	cgt	gat	gca	gtg	cgc	gca	cgg	caa	caa	caa	gcc	aag	gcc	gca	ttc	288
Gln	Arg	Asp	Ala	Val	Arg	Ala	Arg	Gln	Gln	Gln	Ala	Lys	Ala	Ala	Phe	
				85					90					95		
ctt	ccc	cat	gta	tcc	gcc	aat	gac	agc	tac	cag	cgc	cag	ccg	cca	tcg	336
Leu	Pro	His	Val	Ser	Ala	Asn	Ala	Ser	Tyr	Gln	Arg	Gln	Pro	Pro	Ser	
			100					105					110			
att	tct	tcc	acc	cgc	gaa	aca	cag	gga	tgg	agc	gtg	cag	gtg	gga	caa	384
Ile	Ser	Ser	Thr	Arg	Glu	Thr	Gln	Gly	Trp	Ser	Val	Gln	Val	Gly	Gln	
		115					120					125				
acc	tta	ttt	gac	gct	gcc	aaa	ttt	gca	caa	tac	cgc	caa	agc	agg	ttc	432
Thr	Leu	Phe	Asp	Ala	Ala	Lys	Phe	Ala	Gln	Tyr	Arg	Gln	Ser	Arg	Phe	
	130					135					140					
gac	acg	cag	gct	gca	gaa	cag	cgt	tcc	gat	gcg	gca	cgc	gaa	gaa	ttg	480
Asp	Thr	Gln	Ala	Ala	Glu	Gln	Arg	Phe	Asp	Ala	Ala	Arg	Glu	Glu	Leu	
	145				150					155				160		
ctg	tgg	aaa	ggt	gcc	gaa	agt	tat	tcc	aac	ggt	tta	ctc	agc	cga	gac	528
Leu	Leu	Lys	Val	Ala	Glu	Ser	Tyr	Phe	Asn	Val	Leu	Leu	Ser	Arg	Asp	
			165						170					175		
acc	ggt	gcc	gcc	cat	gcg	gcg	gaa	aaa	gag	gct	tat	gcc	cag	cag	gta	576
Thr	Val	Ala	Ala	His	Ala	Ala	Glu	Lys	Glu	Ala	Tyr	Ala	Gln	Gln	Val	
			180					185					190			
agg	cag	gcg	cag	gct	tta	ttc	aat	aaa	ggt	gct	gcc	acc	gcg	ctg	gat	624
Arg	Gln	Ala	Gln	Ala	Leu	Phe	Asn	Lys	Gly	Ala	Ala	Thr	Ala	Leu	Asp	
		195					200					205				
att	cac	gaa	gcc	aaa	gcc	ggt	tac	gac	aat	gcc	ctg	gcc	caa	gaa	acc	672
Ile	His	Glu	Ala	Lys	Ala	Gly	Tyr	Asp	Asn	Ala	Leu	Ala	Gln	Glu	Ile	
	210					215					220					
gcc	gta	ttg	gct	gag	aaa	caa	acc	tat	gaa	aac	cag	ttg	aac	gac	tac	720
Ala	Val	Leu	Ala	Glu	Lys	Gln	Thr	Tyr	Glu	Asn	Gln	Leu	Asn	Asp	Tyr	
	225				230					235				240		
acc	gac	ctg	gat	agc	aaa	caa	atc	gag	gcc	ata	gat	acc	gcc	aac	ctg	768
Thr	Asp	Leu	Asp	Ser	Lys	Gln	Ile	Glu	Ala	Ile	Asp	Thr	Ala	Asn	Leu	
				245					250					255		
ttg	gca	cgc	tat	ctg	ccc	aag	ctg	gaa	cgt	tac	agt	ctg	gat	gaa	tgg	816
Leu	Ala	Arg	Tyr	Leu	Pro	Lys	Leu	Glu	Arg	Tyr	Ser	Leu	Asp	Glu	Trp	
			260					265					270			
cag	cgc	att	gcc	tta	tcc	aac	aat	cat	gaa	tac	cgg	atg	cag	cag	ctt	864

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Gln	Arg	Ile	Ala	Leu	Ser	Asn	Asn	His	Glu	Tyr	Arg	Met	Gln	Gln	Leu		
		275					280					285					
gcc	ctg	caa	agc	agc	gga	cag	gcg	ctt	cgg	gca	gca	cag	aac	agc	cgc	912	
Ala	Leu	Gln	Ser	Ser	Gly	Gln	Ala	Leu	Arg	Ala	Ala	Gln	Asn	Ser	Arg		
		290				295				300							
tat	ccc	acc	gtt	tct	gcc	cat	gtc	ggc	tat	cag	aat	aac	ctc	tac	act	960	
Tyr	Pro	Thr	Val	Ser	Ala	His	Val	Gly	Tyr	Gln	Asn	Asn	Leu	Tyr	Thr		
305					310					315					320		
tca	tct	gcg	cag	aat	aat	gac	tac	cac	tat	cgg	ggc	aaa	ggg	atg	agc	1008	
Ser	Ser	Ala	Gln	Asn	Asp	Tyr	His	Tyr	Arg	Gly	Lys	Gly	Met	Ser			
				325				330					335				
gtc	ggc	gta	cag	ttg	aat	ttg	ccg	ctt	tat	acc	ggc	gga	gaa	ttg	tcg	1056	
Val	Gly	Val		Gln	Leu	Asn	Leu	Pro	Leu	Tyr	Thr	Gly	Gly	Leu	Ser		
				340				345					350				
ggc	aaa	atc	cat	gaa	gcc	gaa	gcg	caa	tac	ggg	gcc	gcc	gaa	gca	cag	1104	
Gly	Lys	Ile	His	Glu	Ala	Glu	Ala	Gln	Tyr	Gly	Ala	Ala	Glu	Ala	Gln		
		355				360						365					
ctg	acc	gca	acc	gag	cgg	cac	atc	aaa	ctc	gcc	gta	cgc	cag	gct	tat	1152	
Leu	Thr	Ala	Thr	Glu	Arg	His	Ile	Lys	Leu	Ala	Val	Arg	Gln	Ala	Tyr		
		370				375					380						
acc	gaa	agc	ggc	gcg	gcg	cgt	tac	caa	atc	atg	gcg	caa	gaa	cgg	gtt	1200	
Thr	Glu	Ser	Gly	Ala	Ala	Arg	Tyr	Gln	Ile	Met	Ala	Gln	Glu	Arg	Val		
385					390					395					400		
ttg	gaa	agc	agc	cgt	ttg	aaa	ctg	aaa	tcg	acc	gaa	acc	ggc	caa	caa	1245	
Leu	Glu	Ser	Ser	Arg	Leu	Lys	Leu	Lys	Ser	Thr	Glu	Thr	Gly	Gln	Gln		
				405				410					415				
tac	ggc	atc	cgc	aac	cgg	ctg	gaa	gta	ata	cgg	gcg	cgg	cag	gaa	gtc	1296	
Tyr	Gly	Ile	Arg	Asn	Arg	Leu	Glu	Val	Ile	Arg	Ala	Arg	Gln	Glu	Val		
			420				425					430					
gcc	caa	gca	gaa	cag	aaa	ctg	gct	caa	gca	cgg	tat	aaa	ttc	atg	ctg	1344	
Ala	Gln	Ala	Glu	Gln	Lys	Leu	Ala	Gln	Ala	Arg	Tyr	Lys	Phe	Met	Leu		
		435				440					445						
gct	tat	ttg	cgc	ttg	gtg	aaa	gag	agc	ggg	tta	ggg	ttg	gaa	acg	gta	1392	
Ala	Tyr	Leu	Arg	Leu	Val	Lys	Glu	Ser	Gly	Leu	Gly	Leu	Glu	Thr	Val		
		450				455				460							
ttt	gcg	gaa	taa													1404	
Phe	Ala	Glu															
465																	

<210> 69  
 <211> 467  
 <212> PRT  
 <213> Neisseria meningitidis

<400> 69  
 Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val  
 1 5 10 15

00830433.001604

Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met  
 20 25 30  
 Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu  
 35 40 45  
 Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala  
 50 55 60  
 Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr  
 65 70 75 80  
 Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe  
 85 90 95  
 Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser  
 100 105 110  
 Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln  
 115 120 125  
 Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe  
 130 135 140  
 Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu  
 145 150 155 160  
 Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp  
 165 170 175  
 Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val  
 180 185 190  
 Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp  
 195 200 205  
 Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile  
 210 215 220  
 Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr  
 225 230 235 240  
 Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu  
 245 250 255  
 Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp  
 260 265 270  
 Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu  
 275 280 285  
 Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg  
 290 295 300  
 Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr  
 305 310 315 320  
 Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser  
 325 330 335

090300Z FEB 60

Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser  
340 345 350

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln  
355 360 365

Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr  
370 375 380

Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val  
385 390 395 400

Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln  
405 410 415

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val  
420 425 430

Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu  
435 440 445

Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val  
450 455 460

Phe Ala Glu  
465

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<211> 696  
<212> DNA  
<213> Neisseria gonorrhoeae

<220>  
<221> CDS  
<222> (1)..(693)

<400> 70  
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Met Lys Gln Ser Ala Arg Ile Lys Asn Met Asp Gln Thr Leu Lys Asn  
1 5 10 15

aca ttg ggc att tgc gcc att tta gcc tta tgt ttt ggc gcc gcc atc 96  
Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile  
20 25 30

gca tca ggt tat cac ttg gaa tat gaa tac gcc tac cgt tat tct gcc 144  
Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala  
35 40 45

gtg ggc gct ttg gct tgc gtt gta ttt tta tta tta ttg gca cgc gcc 192  
Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly  
50 55 60

ttc cag cgc gtt tct tca gtt gtt tta ctg att tac gtc gcc aca acc 240  
Phe Pro Arg Val Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr  
65 70 75 80

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gcc cta tat ttg ccg gtc ggc tgg ctg tat ggt gcg cct tct tat cag 288  
Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln  
85 90 95

ata gtc ggt tgc ata ttg gaa agc aat cct gcc gag gcg cgt gaa ttt 336  
Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe  
100 105 110

gtc ggc aat ctt ccc ggg tgc ctt tat ttt gtg cag gca tta ttt ttc 384  
Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe  
115 120 125

att ttt ggc ttg aca gtc tgg aaa tat tgt gta tct gtg ggg gta ttt 432  
Ile Phe Gly Leu Thr Val Trp Lys Tyr Cys Val Ser Val Gly Val Phe  
130 135 140

gct gac gta aaa aac tat aaa cgt cgc agc aaa ata tgg ctg acc ata 480  
Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile  
145 150 155 160

tta ttg act ttg att ttg tcc tgc gcg ggc atg gag aaa atc gcc ggc 528  
Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Glu Lys Ile Ala Gly  
165 170 175

gat aaa gat tgg cga gaa cct gat gcc ggc ctg ttg ttg aat att ttc 576  
Asp Lys Asp Trp Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe  
180 185 190

gac ctg tat tac gac ttg gct ttc cgc gcc ggc aca ata tgc cgc caa 624  
Asp Leu Tyr Tyr Asp Leu Ala Phe Arg Ala Gly Thr Ile Cys Arg Gln  
195 200 205

ggc cgc cca cat ttt gga agt agc aaa aaa agc gtc aac atg gca tat 672  
Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr  
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ccg cca act tgc gcc caa gta taa 696  
Pro Pro Thr Cys Ala Gln Val  
225 230

<210> 71  
<211> 231  
<212> PRT  
<213> Neisseria gonorrhoeae

<400> 71  
Met Lys Gln Ser Ala Arg Ile Lys Asn Met Asp Gln Thr Leu Lys Asn  
1 5 10 15

Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile  
20 25 30

Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala  
35 40 45

Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly  
50 55 60

Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr

09030433-081601

65	70	75	80
Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln			
85		90	95
Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe			
100	105		110
Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe			
115	120		125
Ile Phe Gly Leu Thr Val Trp Lys Tyr Cys Val Ser Val Gly Val Phe			
130	135		140
Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile			
145	150	155	160
Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Glu Lys Ile Ala Gly			
165	170		175
Asp Lys Asp Trp Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe			
180	185		190
Asp Leu Tyr Tyr Asp Leu Ala Phe Arg Ala Gly Thr Ile Cys Arg Gln			
195	200		205
Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr			
210	215		220
Pro Pro Thr Cys Ala Gln Val			
225	230		

<210> 72  
 <211> 2607  
 <212> DNA  
 <213> Neisseria meningitidis

<220>  
 <221> CDS  
 <222> (1)..(2604)

<400> 72  
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 Met Ala Ala Asn Gln Arg Tyr Arg Lys Pro Leu Pro Gly Thr Asp Leu  
 1 5 10 15  
 gaa tac tac gac gcg cgt gcg gcg tgt gag ggc atc aaa ccc gcc tct 96  
 Glu Tyr Tyr Ala Arg Ala Ala Cys Glu Gly Ile Lys Pro Gly Ser  
 20 25 30  
 tac gac aag ctg cct tac acg agc cgc att ttg gcg gag aat ttg gtc 144  
 Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val  
 35 40 45  
 aac cgc gcg gac aaa gtc gat ttg cgc acg ctg caa agc tgg ctg ggt 192  
 Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly  
 50 55 60

009180-EE40E360

cag ctg att gag gga aaa cag gaa atc gac ttt cct tgg tat ccg gcg	240
Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala	
65 70 75 80	
cgg gtg gtg tgc cac gat att ctg ggg cag acc gcg ttg gtg gat ttg	288
Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu	
85 90 95	
gca ggt ctg cgc gat gcg att gcc gaa aaa ggc ggc gat cct gcc aaa	336
Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys	
100 105 110	
gtg aat ccg gtg gtg caa acc cag ctc atc gtc gac cac tcg ctg gcg	384
Val Asn Pro Val Val Gln Thr Gln Leu Ile Val Asp His Ser Leu Ala	
115 120 125	
gtg gaa tgc ggc ggc tac gac ccc gat gcg ttc cgc aaa aac cgc gaa	432
Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg Glu	
130 135 140	
atc gaa gac aga cgt aac gaa gac cgt ttc cac ttc atc aac tgg aca	480
Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp Thr	
145 150 155 160	
aaa acc gcc ttt gaa aat gtg gac gtg att ccg gcg ggc aac ggc atc	528
Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly Ile	
165 170 175	
atg cac caa atc aat cta gaa aaa atg tgg ccc gtc gtc caa gtc aaa	576
Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val Lys	
180 185 190	
aac ggc gtg gcc ttc ccc gat acc tgc gtc ggc acg gat tcg cac acg	624
Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His Thr	
195 200 205	
cca cac gtc gat gcg ctg ggc gtg att ttc gtg ggc gtg ggc gga ttg	672
Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly Leu	
210 215 220	
gaa gcg gaa acc gta atg ctg gga cgc gcg tcc atg atg cgc ctg ccc	720
Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu Pro	
225 230 235 240	
gat att gtc ggc gtt gag ctg aac ggc aaa cgg aag gcg ggc att acg	768
Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Lys Ala Gly Ile Thr	
245 250 255	
gcg acg gat att gtg ttg gca ctg acc gag ttc ctg cgc aaa gaa cgc	816
Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu Arg	
260 265 270	
gtg gtc ggg gcg ttt gcc gaa ttc ttc ggc gag ggc gcg aga agc ctg	864
Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser Leu	
275 280 285	
tct atc ggc gac cgc gcg acc att tcc aac atg acg ccg gag ttc ggc	912
Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe Gly	
290 295 300	



att gaa aac gac gta ctc ggc gtt gca gac ggc aaa gaa atc cgc ctg Ile Glu Asn Asp Val Leu Gly Val Ala Asp Gly Lys Glu Ile Arg Leu 545 550 555 560	1680
aaa gac att tgg cct acc gat gaa gaa atc gat gcc atc gtt gcc gaa Lys Asp Ile Trp Pro Thr Asp Glu Glu Ile Asp Ala Ile Val Ala Glu 565 570 575	1728
tat gtg aaa ccg cag caa ttt cgc gac gtt tat atc ccg atg ttc gac Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Ile Pro Met Phe Asp 580 585 590	1776
acc ggc aca gcg caa aaa gca cca agc ccg ctg tac gac tgg cgt cca Thr Gly Thr Ala Gln Lys Ala Pro Ser Pro Leu Tyr Asp Trp Arg Pro 595 600 605	1824
atg tct acc tat atc cgc cgc cca cct tac tgg gaa ggc gca ctg gca Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu Ala 610 615 620	1872
ggg gaa cgc aca tta agc ggt atg cgt ccg ctg gcg att ttg ccc gac Gly Glu Arg Thr Leu Ser Gly Met Arg Pro Leu Ala Ile Leu Pro Asp 625 630 635 640	1920
aac atc acc acc gac cat ctc tcg cca tcc aat gcg att ttg gca agc Asn Ile Thr Thr Asp His Leu Ser Pro Ser Asn Ala Ile Leu Ala Ser 645 650 655	1968
agt gcc gca ggc gaa tat ttg gca aaa atg ggt ttg cct gaa gaa gac Ser Ala Ala Gly Glu Tyr Leu Ala Lys Met Gly Leu Pro Glu Glu Asp 660 665 670	2016
ttc aac tct tac gca acc cac cgt ggc gac cac ttg acc gcc caa cgc Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln Arg 675 680 685	2064
gca acc ttc gcc aat ccg aaa ctg ttt aac gaa atg gtg aga aac gaa Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Arg Asn Glu 690 695 700	2112
gac ggc agc gta cgc caa ggt tcg ctg gca cgc gtt gaa ccc gaa ggc Asp Gly Ser Val Arg Gln Gly Ser Leu Ala Arg Val Glu Pro Glu Gly 705 710 715 720	2160
caa acc atg cgc atg tgg gaa gcc atc gaa acc tat atg aac cgc aaa Gln Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg Lys 725 730 735	2208
cag ccg ctc atc atc att gcc ggc gcg gac tac ggt caa ggc tca agc Gln Pro Leu Ile Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser Ser 740 745 750	2256
cgc gac tgg gct gca aaa ggc gta cgc ctc gcc ggc gtg gaa gcg att Arg Asp Trp Ala Ala Lys Gly Val Arg Leu Ala Gly Val Glu Ala Ile 755 760 765	2304
gtt gcc gaa ggc ttc gag cgt atc cac cgc acc aac ttg atc ggt atg Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly Met 770 775 780	2352

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ggc gtg ttg ccg ctg cag ttc aaa ccg ggt acc aac cgc cac acc ctg 2400
Gly Val Leu Pro Leu Gln Phe Lys Pro Gly Thr Asn Arg His Thr Leu
785              790              795              800

caa ctg gac ggt acg gaa acc tac gac gtt gtc ggc gaa cgc aca ccg 2448
Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr Pro
              805              810              815

cgc tgc gac ctg acc ctt gtg att cac cgt aaa aac ggc gag acc gtc 2496
Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr Val
              820              825              830

gaa gtc ccc att acc tgc cgc ctc gat acc gca gaa gaa gtg ttg gta 2544
Glu Val Pro Ile Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu Val
              835              840              845

tat gaa gcc ggt ggc gta ttg caa cgg ttt gca cag gat ttt ttg gaa 2592
Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu Glu
              850              855              860

ggg aac gcg gct tag 2607
Gly Asn Ala Ala
865

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<210> 73  
 <211> 868  
 <212> PRT  
 <213> Neisseria meningitidis

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<400> 73
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Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Gly Ile Lys Pro Gly Ser
              20              25              30

Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val
              35              40              45

Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly
              50              55              60

Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala
              65              70              75              80

Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu
              85              90              95

Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys
              100              105              110

Val Asn Pro Val Val Gln Thr Gln Leu Ile Val Asp His Ser Leu Ala
              115              120              125

Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg Glu
              130              135              140

Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp Thr
              145              150              155              160

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09030433-084604

Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly Ile  
 165 170 175  
 Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val Lys  
 180 185 190  
 Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His Thr  
 195 200 205  
 Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly Leu  
 210 215 220  
 Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu Pro  
 225 230 235 240  
 Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Lys Ala Gly Ile Thr  
 245 250 255  
 Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu Arg  
 260 265 270  
 Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser Leu  
 275 280 285  
 Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe Gly  
 290 295 300  
 Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr Leu  
 305 310 315 320  
 Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr Tyr  
 325 330 335  
 Ala Lys Thr Ala Gly Leu Trp Ala Asp Ala Leu Lys Thr Ala Val Tyr  
 340 345 350  
 Pro Arg Val Leu Lys Phe Asp Leu Ser Ser Val Thr Arg Asn Met Ala  
 355 360 365  
 Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala Gly  
 370 375 380  
 Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met Pro  
 385 390 395 400  
 Asp Gly Ala Val Ile Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr Ser  
 405 410 415  
 Asn Pro Arg Asn Val Val Ala Ala Ala Leu Leu Ala Arg Asn Ala Asn  
 420 425 430  
 Arg Leu Gly Leu Gln Arg Lys Pro Trp Val Lys Ser Ser Phe Ala Pro  
 435 440 445  
 Gly Ser Lys Val Ala Glu Ile Tyr Leu Lys Glu Ala Asp Leu Leu Pro  
 450 455 460  
 Glu Met Glu Lys Leu Gly Phe Gly Ile Val Ala Phe Ala Cys Thr Thr  
 465 470 475 480

09830433-084604

Cys	Asn	Gly	Met	Ser	Gly	Ala	Leu	Asp	Pro	Lys	Ile	Gln	Lys	Glu	Ile	485	490	495
Ile	Asp	Arg	Asp	Leu	Tyr	Ala	Thr	Ala	Val	Leu	Ser	Gly	Asn	Arg	Asn	500	505	510
Phe	Asp	Gly	Arg	Ile	His	Pro	Tyr	Ala	Lys	Gln	Ala	Phe	Leu	Ala	Ser	515	520	525
Pro	Pro	Leu	Val	Val	Ala	Tyr	Ala	Leu	Ala	Gly	Ser	Ile	Arg	Phe	Asp	530	535	540
Ile	Glu	Asn	Asp	Val	Leu	Gly	Val	Ala	Asp	Gly	Lys	Glu	Ile	Arg	Leu	545	550	555
Lys	Asp	Ile	Trp	Pro	Thr	Asp	Glu	Glu	Ile	Asp	Ala	Ile	Val	Ala	Glu	565	570	575
Tyr	Val	Lys	Pro	Gln	Gln	Phe	Arg	Asp	Val	Tyr	Ile	Pro	Met	Phe	Asp	580	585	590
Thr	Gly	Thr	Ala	Gln	Lys	Ala	Pro	Ser	Pro	Leu	Tyr	Asp	Trp	Arg	Pro	595	600	605
Met	Ser	Thr	Tyr	Ile	Arg	Arg	Pro	Pro	Tyr	Trp	Glu	Gly	Ala	Leu	Ala	610	615	620
Gly	Glu	Arg	Thr	Leu	Ser	Gly	Met	Arg	Pro	Leu	Ala	Ile	Leu	Pro	Asp	625	630	635
Asn	Ile	Thr	Thr	Asp	His	Leu	Ser	Pro	Ser	Asn	Ala	Ile	Leu	Ala	Ser	645	650	655
Ser	Ala	Ala	Gly	Glu	Tyr	Leu	Ala	Lys	Met	Gly	Leu	Pro	Glu	Glu	Asp	660	665	670
Phe	Asn	Ser	Tyr	Ala	Thr	His	Arg	Gly	Asp	His	Leu	Thr	Ala	Gln	Arg	675	680	685
Ala	Thr	Phe	Ala	Asn	Pro	Lys	Leu	Phe	Asn	Glu	Met	Val	Arg	Asn	Glu	690	695	700
Asp	Gly	Ser	Val	Arg	Gln	Gly	Ser	Leu	Ala	Arg	Val	Glu	Pro	Glu	Gly	705	710	715
Gln	Thr	Met	Arg	Met	Trp	Glu	Ala	Ile	Glu	Thr	Tyr	Met	Asn	Arg	Lys	725	730	735
Gln	Pro	Leu	Ile	Ile	Ile	Ala	Gly	Ala	Asp	Tyr	Gly	Gln	Gly	Ser	Ser	740	745	750
Arg	Asp	Trp	Ala	Ala	Lys	Gly	Val	Arg	Leu	Ala	Gly	Val	Glu	Ala	Ile	755	760	765
Val	Ala	Glu	Gly	Phe	Glu	Arg	Ile	His	Arg	Thr	Asn	Leu	Ile	Gly	Met	770	775	780
Gly	Val	Leu	Pro	Leu	Gln	Phe	Lys	Pro	Gly	Thr	Asn	Arg	His	Thr	Leu	785	790	795

TOPTBO"EE40E350

Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr Pro  
805 810 815

Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr Val  
820 825 830

Glu Val Pro Ile Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu Val  
835 840 845

Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu Glu  
850 855 860

Gly Asn Ala Ala  
865

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<212> DNA  
<213> Neisseria meningitidis

<220>  
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<222> (1)..(1167)

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Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu  
20 25 30

gcg gga agc gca cgc gac aaa atc ctc ttg cgc gta ctc ggc agc ccg 144  
Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro  
35 40 45

gat ccc tac ggc aag cag ata gac ggt ttg ggc aac gcc agc tcg tcc 192  
Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser  
50 55 60

acc agc aag gcg gtg att ttg gac aag tcc gaa cgc gcc gat cac gat 240  
Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Ala Asp His Asp  
65 70 75 80

gtc gat tac ctt ttc ggg caa gtt tcc atc gac aaa cct ttt gtc gat 288  
Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp  
85 90 95

tgg agt ggc aac tgc ggc aac ctc acc gcc gcc gtg ggc gca ttt gcc 336  
Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala  
100 105 110

atc gag caa ggc ttg gtc gat aaa ggc aag att cct tca gac ggc atc 384  
Ile Glu Gln Gly Leu Val Asp Lys Gly Lys Ile Pro Ser Asp Gly Ile  
115 120 125

09830433-081601

tcg	aca	gtc	aaa	atc	tgg	cag	aaa	aac	atc	ggc	aaa	acc	att	att	gcc	432
Cys	Thr	Val	Lys	Ile	Trp	Gln	Lys	Asn	Ile	Gly	Lys	Thr	Ile	Ile	Ala	
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cat	gta	ccg	atg	caa	aac	ggc	gca	gtt	tgg	gaa	aca	ggc	gat	ttt	gag	480
His	Val	Pro	Met	Gln	Asn	Gly	Ala	Val	Leu	Glu	Thr	Gly	Asp	Phe	Glu	
145					150					155					160	
ctc	gac	ggc	gta	acg	ttc	ccg	gca	gcc	gaa	gta	caa	atc	gaa	ttt	ctt	528
Leu	Asp	Gly	Val	Thr	Phe	Pro	Ala	Ala	Glu	Val	Gln	Ile	Glu	Phe	Leu	
				165					170					175		
gat	cca	gcc	gac	ggc	gaa	ggc	agt	atg	ttc	cca	acc	ggc	aat	ttg	gtc	576
Asp	Pro	Ala	Asp	Gly	Glu	Gly	Ser	Met	Phe	Pro	Thr	Gly	Asn	Leu	Val	
			180					185					190			
gat	gaa	att	gat	gtg	ccg	aat	ata	ggc	cgt	ttg	aaa	gcc	acg	ctc	atc	624
Asp	Glu	Ile	Asp	Val	Pro	Asn	Ile	Gly	Arg	Leu	Lys	Ala	Thr	Leu	Ile	
		195					200					205				
aac	gcg	ggc	att	ccg	acc	gtt	ttc	ctg	aat	gcc	gcc	gac	ttg	ggc	tac	672
Asn	Ala	Gly	Ile	Pro	Thr	Val	Phe	Leu	Asn	Ala	Ala	Asp	Leu	Gly	Tyr	
	210					215					220					
acg	ggc	aaa	gag	ttg	caa	gac	gac	atc	aac	aac	gat	gcc	gca	gct	ttg	720
Thr	Gly	Lys	Glu	Leu	Gln	Asp	Asp	Ile	Asn	Asn	Asp	Ala	Ala	Ala	Leu	
225					230					235					240	
gaa	aaa	ttc	gag	aaa	atc	cgc	gct	tac	ggg	gcg	ctg	aaa	atg	ggg	ctg	768
Glu	Lys	Phe	Glu	Lys	Ile	Arg	Ala	Tyr	Gly	Ala	Leu	Lys	Met	Gly	Leu	
				245					250					255		
atc	agc	gac	gta	tcc	gaa	gct	gcc	gcc	cgc	gcg	cac	acg	ccg	aaa	gtc	816
Ile	Ser	Asp	Val	Ser	Glu	Ala	Ala	Ala	Arg	Ala	His	Thr	Pro	Lys	Val	
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gcc	ttc	gtc	gcg	ccc	gcc	gcc	gat	tac	acc	gcc	tcc	agt	ggc	aaa	acc	864
Ala	Phe	Val	Ala	Pro	Ala	Ala	Asp	Tyr	Thr	Ala	Ser	Ser	Gly	Lys	Thr	
		275					280					285				
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Val	Asn	Ala	Ala	Asp	Ile	Asp	Leu	Leu	Val	Arg	Ala	Leu	Ser	Met	Gly	
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aaa	ttg	cac	cac	gcg	atg	atg	ggg	acc	gcc	tct	gtt	gcc	att	gcg	acc	960
Lys	Leu	His	His	Ala	Met	Met	Gly	Thr	Ala	Ser	Val	Ala	Ile	Ala	Thr	
305					310					315					320	
gcc	gcc	gcc	gtg	ccc	ggg	acg	ctg	gtc	aac	ctt	gcc	gca	ggc	ggc	gga	1008
Ala	Ala	Ala	Val	Pro	Gly	Thr	Leu	Val	Asn	Leu	Ala	Ala	Gly	Gly	Gly	
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			20					25					30				
Ala	Gly	Ser	Ala	Arg	Asp	Lys	Ile	Leu	Leu	Arg	Val	Leu	Gly	Ser	Pro		
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Asp	Pro	Tyr	Gly	Lys	Gln	Ile	Asp	Gly	Leu	Gly	Asn	Ala	Ser	Ser	Ser		
	50					55					60						
Thr	Ser	Lys	Ala	Val	Ile	Leu	Asp	Lys	Ser	Glu	Arg	Ala	Asp	His	Asp		
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Val	Asp	Tyr	Leu	Phe	Gly	Gln	Val	Ser	Ile	Asp	Lys	Pro	Phe	Val	Asp		
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Trp	Ser	Gly	Asn	Cys	Gly	Asn	Leu	Thr	Ala	Ala	Val	Gly	Ala	Phe	Ala		
			100					105					110				
Ile	Glu	Gln	Gly	Leu	Val	Asp	Lys	Gly	Lys	Ile	Pro	Ser	Asp	Gly	Ile		
		115					120					125					
Cys	Thr	Val	Lys	Ile	Trp	Gln	Lys	Asn	Ile	Gly	Lys	Thr	Ile	Ile	Ala		
	130					135					140						
His	Val	Pro	Met	Gln	Asn	Gly	Ala	Val	Leu	Glu	Thr	Gly	Asp	Phe	Glu		
	145				150					155					160		
Leu	Asp	Gly	Val	Thr	Phe	Pro	Ala	Ala	Glu	Val	Gln	Ile	Glu	Phe	Leu		
				165					170					175			
Asp	Pro	Ala	Asp	Gly	Glu	Gly	Ser	Met	Phe	Pro	Thr	Gly	Asn	Leu	Val		
			180					185					190				
Asp	Glu	Ile	Asp	Val	Pro	Asn	Ile	Gly	Arg	Leu	Lys	Ala	Thr	Leu	Ile		
		195					200					205					
Asn	Ala	Gly	Ile	Pro	Thr	Val	Phe	Leu	Asn	Ala	Ala	Asp	Leu	Gly	Tyr		
	210					215					220						
Thr	Gly	Lys	Glu	Leu	Gln	Asp	Asp	Ile	Asn	Asn	Asp	Ala	Ala	Ala	Leu		
	225				230					235					240		

Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu  
 245 250 255  
 Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val  
 260 265 270  
 Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr  
 275 280 285  
 Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly  
 290 295 300  
 Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr  
 305 310 315 320  
 Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Gly Gly  
 325 330 335  
 Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val  
 340 345 350  
 Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala  
 355 360 365  
 Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val  
 370 375 380  
 Pro Glu Asp Cys Phe  
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<210> 76  
 <211> 2094  
 <212> DNA  
 <213> Neisseria gonorrhoeae

<220>  
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 <222> (1)..(2091)

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 ttc gcc tct ggc ttc tgc gcc ctg att tac cag gtc agc tgg cag agg 96  
 Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg  
 20 25 30  
 ctt cta ttc agc cac ata ggt atc gat ttg agt tcg att act gtc att 144  
 Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile  
 35 40 45  
 att tct gta ttt atg gtc ggc ttg ggt gta ggt gcg tat ttc ggc gga 192  
 Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly  
 50 55 60  
 cgc att gct gac cgt ttt cct tca agt atc atc ccc ctg ttt tgc atc 240  
 Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile

09030433 081504

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gct gaa gta tcc atc ggt ctg ttc ggt ttg gta agc aag ggt ctg att	288															
Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Lys Gly Leu Ile																
85 90 95																
tcc ggc ttg ggg cat ctt tta gtt gag gct gat ttg ccc atc atc gct	336															
Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala																
100 105 110																
gct gcc aat ttc ctc tta ttg ctg ctt cct acc ttt atg atg ggc gcg	384															
Ala Ala Asn Phe Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala																
115 120 125																
acc ttg ccc ttg ctg acc tgt ttt ttt aac cgg aaa ata cat aat gtt	432															
Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val																
130 135 140																
ggc gag tct atc ggt acc tta tat ttt ttc aac act ttg ggt gcg gca	480															
Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala																
145 150 155 160																
ctc gga tgc ctt gcc gcc gcc gaa ttt ttc tac gtc ttt ttt acc ctc	528															
Leu Gly Ser Leu Ala Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu																
165 170 175																
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Ser Gln Thr Ile Ala Leu Thr Ala Cys Leu Asn Leu Leu Ile Ala Ala																
180 185 190																
tca gta tgc tgc gtt aca gaa agg atg gat atg gtg aac act aaa ccg	624															
Ser Val Cys Cys Val Thr Glu Arg Met Asp Met Val Asn Thr Lys Pro																
195 200 205																
aat act agt gtg att aat atg ctt tct ttc ctt acc gga tta ttg agc	672															
Asn Thr Ser Val Ile Asn Met Leu Ser Phe Leu Thr Gly Leu Leu Ser																
210 215 220																
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225 230 235 240																
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Ser Val Pro Gln Ala Phe Ser Phe Ile Leu Ala Cys Phe Leu Thr Gly																
245 250 255																
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Ile Ala Val Gly Ala Tyr Phe Gly Lys Arg Ile Cys Arg Ser Arg Phe																
260 265 270																
gtt gat att ccc ttt atc ggg cag tgc ttc ttg tgg gcg ggt att gcc	864															
Val Asp Ile Pro Phe Ile Gly Gln Cys Phe Leu Trp Ala Gly Ile Ala																
275 280 285																
gat ttt ttg att ttg ggt gct gcg tgg ttg ttg acg ggt ttt tcc ggt	912															
Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly																
290 295 300																
ttc gtc cac cac gcc ggt att ttc att acc ctg tct gcc gtc gtc agg	960															
Phe Val His His Ala Gly Ile Phe Ile Thr Leu Ser Ala Val Val Arg																

305	310	315	320	
ggg ttg att ttc cca ctt gta cac cat gtg ggt acg gat ggc aac aaa				1008
Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys				
325		330	335	
tcc gga cga cag gtt tcc aat gtt tat ttc gcc aac gtt gcc ggc agt				1056
Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser				
340		345	350	
gca ttg ggt ccg gtc ctt atc ggc ttt gtg ata ctt gat ttg ttg tcc				1104
Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Leu Leu Ser				
355		360	365	
acc caa cag att tac ctg ctc atc tgt ttg att tct gct gct gtc cct				1152
Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro				
370		375	380	
ttg ttt tgt aca ctg ttc caa aaa agt ctc cga ctg aat gca gtg tcg				1200
Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser				
385		390	395	400
gta gca gtt tcc cta atg ttc ggc atc ctc atg ttc cta ctg ccg gat				1248
Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp				
405		410	415	
tct gtc ttt caa aat att gct ggc cgt ccg gat agg ttg att gaa aac				1296
Ser Val Phe Gln Asn Ile Ala Gly Arg Pro Asp Arg Leu Ile Glu Asn				
420		425	430	
aaa cac ggc att gtt gcg gtt tac cat aga gat ggt gat aag gtt gtt				1344
Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val				
435		440	445	
tat ggg gcg aat gta tac gac ggc gca tac aat acc gat ata ttc aat				1392
Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Ile Phe Asn				
450		455	460	
agt gtc aac ggc atc gaa cgt gcc tat ctg cta ccc tcc ctg aag tcc				1440
Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser				
465		470	475	480
ggc ata cgc cgc att ttc gtc gtt gga ttg agt aca ggt tcg tgg gcg				1488
Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala				
485		490	495	
cgc gtc ttg tct gcc att ccg gaa atg cag tcg atg atc gtt gcg gaa				1536
Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu				
500		505	510	
atc aat ccg gca tac cgt agc ctt atc gcg gac gag ccg caa atc gca				1584
Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala				
515		520	525	
ccg ctt ttg cag gac aaa cgt gtt gaa att gta ttg gat gac ggt agg				1632
Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg				
530		535	540	
aaa tgg ctg cgt cgc cat cct gat gaa aaa ttc gac ctg att ttg atg				1680
Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met				

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<210> 77
<211> 697
<212> PRT
<213> Neisseria gonorrhoeae
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Met Asn Ser Thr Ala Ser Lys Thr Leu Lys Gly Leu Ser Leu Val Phe
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Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg
      20                               25                      30

Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile
      35                               40                      45

Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly
      50                               55                      60

Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile
      65                               70                      75                      80

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Ala	Glu	Val	Ser	Ile	Gly	Leu	Phe	Gly	Leu	Val	Ser	Lys	Gly	Leu	Ile	85	90	95	
Ser	Gly	Leu	Gly	His	Leu	Leu	Val	Glu	Ala	Asp	Leu	Pro	Ile	Ile	Ala	100	105	110	
Ala	Ala	Asn	Phe	Leu	Leu	Leu	Leu	Leu	Pro	Thr	Phe	Met	Met	Gly	Ala	115	120	125	
Thr	Leu	Pro	Leu	Leu	Thr	Cys	Phe	Phe	Asn	Arg	Lys	Ile	His	Asn	Val	130	135	140	
Gly	Glu	Ser	Ile	Gly	Thr	Leu	Tyr	Phe	Phe	Asn	Thr	Leu	Gly	Ala	Ala	145	150	155	160
Leu	Gly	Ser	Leu	Ala	Ala	Ala	Glu	Phe	Phe	Tyr	Val	Phe	Phe	Thr	Leu	165	170	175	
Ser	Gln	Thr	Ile	Ala	Leu	Thr	Ala	Cys	Leu	Asn	Leu	Leu	Ile	Ala	Ala	180	185	190	
Ser	Val	Cys	Cys	Val	Thr	Glu	Arg	Met	Asp	Met	Val	Asn	Thr	Lys	Pro	195	200	205	
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Leu	Gly	Ile	Glu	Val	Leu	Trp	Val	Arg	Met	Phe	Ser	Phe	Ala	Ala	Gln	225	230	235	240
Ser	Val	Pro	Gln	Ala	Phe	Ser	Phe	Ile	Leu	Ala	Cys	Phe	Leu	Thr	Gly	245	250	255	
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Val	Asp	Ile	Pro	Phe	Ile	Gly	Gln	Cys	Phe	Leu	Trp	Ala	Gly	Ile	Ala	275	280	285	
Asp	Phe	Leu	Ile	Leu	Gly	Ala	Ala	Trp	Leu	Leu	Thr	Gly	Phe	Ser	Gly	290	295	300	
Phe	Val	His	His	Ala	Gly	Ile	Phe	Ile	Thr	Leu	Ser	Ala	Val	Val	Arg	305	310	315	320
Gly	Leu	Ile	Phe	Pro	Leu	Val	His	His	Val	Gly	Thr	Asp	Gly	Asn	Lys	325	330	335	
Ser	Gly	Arg	Gln	Val	Ser	Asn	Val	Tyr	Phe	Ala	Asn	Val	Ala	Gly	Ser	340	345	350	
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Thr	Gln	Gln	Ile	Tyr	Leu	Leu	Ile	Cys	Leu	Ile	Ser	Ala	Ala	Val	Pro	370	375	380	
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Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp  
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Ser Val Phe Gln Asn Ile Ala Gly Arg Pro Asp Arg Leu Ile Glu Asn  
420 425 430

Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val  
435 440 445

Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Ile Phe Asn  
450 455 460

Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser  
465 470 475 480

Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala  
485 490 495

Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu  
500 505 510

Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala  
515 520 525

Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg  
530 535 540

Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met  
545 550 555 560

Asn Ser Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala  
565 570 575

Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Ile Val  
580 585 590

Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His  
595 600 605

Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala  
610 615 620

Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser  
625 630 635 640

Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr  
645 650 655

Val Asp Ala Ala Ala Gln Lys Val Val Ser Arg Met Leu Ile Arg Met  
660 665 670

Thr Glu Pro Ser Ala Gly Ala Glu Val Ile Thr Asp Asp Asn Met Ile  
675 680 685

Val Glu Tyr Lys Tyr Gly Arg Gly Ile  
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<210> 78

<211> 39

<212> DNA

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096043-00160

<220>

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<220>

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<211> 32

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<220>

<223> Artificial sequence description: PCR primer

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<210> 81

<211> 27

<212> DNA

<213> Artificial sequence

<220>

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109180 66406360

<211> 35

<213> Artificial sequence

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<211> 31

<213> Artificial sequence

<223> Artificial sequence description: PCR primer

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<211> 34

<213> Artificial sequence

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<211> 30

<213> Artificial sequence

<220>

<223> Artificial sequence description: PCR primer

<400> 85

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<210> 86

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: PCR primer

<400> 86

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<210> 87

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: PCR primer

<400> 87

cgggatccag caacggcctg ccgctttaag 30

<210> 88

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: PCR primer

<400> 88

gctctagacc accatgctga cgtttatcgg actg 34

09630433.081504

<210> 89  
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<210> 90  
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<210> 91  
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<210> 92  
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<211> 33  
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<223> Artificial sequence description: PCR primer

<400> 96  
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<210> 97  
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<223> Artificial sequence description: PCR primer

<400> 97  
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<210> 98  
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<223> Artificial sequence description: PCR primer

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090433 081504

<223> Artificial sequence description: PCR primer

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<223> Artificial sequence description: PCR primer

<400> 101

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<223> Artificial sequence description: PCR primer

<400> 102

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<210> 103

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gctctagacc accatgcaaa acggcggggg aaag 34

<210> 105  
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<210> 106  
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<220>  
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<400> 106  
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<210> 107  
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<210> 108  
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<210> 109  
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<220>  
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cgggatccat acttgggcgc aacatgac 28

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gctctagacc accatgaatg tttagcggttt ccc 33

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<210> 117  
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<213> Artificial sequence

<220>

<223> Artificial sequence description: PCR primer

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<210> 119

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<210> 120

<211> 34

<212> DNA

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<223> Artificial sequence description: PCR primer

<400> 120

009130 00403000

gctctagacc accatgccgc aaattaaaat tccc

34

<210> 121

<211> 29

<212> DNA

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<223> Artificial sequence description: PCR primer

<400> 121

cgggatccaa aaacaatctt ccggcaccc

29

<210> 122

<211> 33

<212> DNA

<213> Artificial sequence

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<400> 122

gctctagacc accatgcgca cgccgttttg ttg

33

<210> 123

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<223> Artificial sequence description: PCR primer

<400> 123

cgggatccat tgggcaacga cgaaggcac

29

<210> 124

<211> 33

<212> DNA

<213> Artificial sequence

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<223> Artificial sequence description: PCR primer

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gctctagacc accatgagaa tagagatcac acc 33

<210> 125

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: PCR primer

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<210> 126

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: PCR primer

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gctctagacc accatgattc acgtttcggc agtg 34

<210> 127

<211> 29

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<223> Artificial sequence description: PCR primer

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TCGTCAGACC ACCATGAGAA TAGAGATCAC ACC

<210> 128

<211> 36

<212> DNA

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<223> Artificial sequence description: PCR primer

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<210> 129

<211> 28

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<223> Artificial sequence description: PCR primer

<400> 129

cgggatccaa atccctctgc cgtatttg 28